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TITLE: Prevention of Trauma/Hemorrhagic Shock-Induced Mortality, Apoptosis, Inflammation and Mitochondrial Dysfunction

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14. ABSTRACT- Trauma complicated by hemorrhagic shock (T/HS) on the battlefield is distinct from the civilian arena especially with regards to clinical diagnosis and resuscitation protocols. Progress towards development of new first-responder resuscitation adjuvants for polytrauma and blast injuries that will maintain tissue viability requires that an agent that demonstrates efficacy in animal models that mimic T-HS and resuscitation in the civilian setting also work in animal models of T-HS that mimic combat casualties and battlefield management. We developed a rat T-HS model in which we demonstrated: 1) 72% mortality at 48 hr, 2) hypovolemic circulatory collapse, 3) left ventricular contractile dysfunction, 4) apoptosis of cardiomyocytes, alveolar epithelial cells, hepatocytes and leukocytes, 5) organ inflammation, 6) organ-specific alterations in the apoptosis transcriptome and 7) increased susceptibility to bacterial infections. Especially notable was the finding that apoptosis and inflammation required resuscitation. Remarkably, use of IL-6 (10 ug/kg) as a resuscitation adjuvant: 1) reduced mortality 5 fold, 2) prevented hypovolemic circulatory collapse, 3) prevented ventricular contractile dysfunction, 4) prevented apoptosis of cardiomyocytes, alveolar epithelial cells, hepatocytes and leukocytes, 5) reduced organ inflammation, 6) normalized the apoptosis and inflammation transcriptome in the heart, lung and liver and 7) reduced T-HS-mediated increased susceptibility to bacterial infections. Importantly from a mechanistic standpoint, results using a pharmacological inhibitor of Stat3 and mice deficient in Stat3□, a dominant-negative isoform of Stat3, demonstrated that virtually all of the beneficial effects of IL-6 were mediated through Stat3 especially Stat3□, which, in addition to its transcriptional role in the nucleus, recently has been demonstrated to support oxidative phosphorylation within mitochondria. Based on these findings (2-6), we hypothesize that IL-6 administration at the start of resuscitation will be beneficial to rats and swine subjected to polytrauma and HS models that more closely mimic battlefield injuries and resuscitation protocols and that IL-6 merits consideration as a resuscitation adjuvant for use by medics at the time of Hextend administration to soldiers suffering from T-HS.

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INTRODUCTION:

Trauma complicated by hemorrhagic shock (T/HS) on the battlefield is distinct from the civilian arena especially with regards to clinical diagnosis and resuscitation protocols. Progress towards development of new first-responder resuscitation adjuvants for polytrauma and blast injuries that will maintain tissue viability requires that an agent that demonstrates efficacy in animal models that mimic T-HS and resuscitation in the civilian setting also work in animal models of T-HS that mimic combat casualties and battlefield management. We developed a rat T-HS model in which we demonstrated: 1) 72% mortality at 48 hr, 2) hypovolemic circulatory collapse, 3) left ventricular contractile dysfunction, 4) apoptosis of cardiomyocytes, alveolar epithelial cells, hepatocytes and leukocytes, 5) organ inflammation, 6) organ-specific alterations in the apoptosis transcriptome and 7) increased susceptibility to bacterial infections. Especially notable was the finding that apoptosis and inflammation required resuscitation. Remarkably, use of IL-6 (10 ug/kg) as a resuscitation adjuvant: 1) reduced mortality 5 fold, 2) prevented hypovolemic circulatory collapse, 3) prevented ventricular contractile dysfunction, 4) prevented apoptosis of cardiomyocytes, alveolar epithelial cells, hepatocytes and leukocytes, 5) reduced organ inflammation, 6) normalized the apoptosis and inflammation transcriptome in the heart, lung and liver and 7) reduced T-HS-mediated increased susceptibility to bacterial infections. Importantly from a mechanistic standpoint, results using a pharmacological inhibitor of Stat3 and mice deficient in Stat3β, a dominant-negative isoform of Stat3, demonstrated that virtually all of the beneficial effects of IL-6 were mediated through Stat3 especially Stat3α, which, in addition to its transcriptional role in the nucleus, recently has been demonstrated to support oxidative phosphorylation within mitochondria. Based on these findings (2-6), we hypothesize that IL-6 administration at the start of resuscitation will be beneficial to rats and swine subjected to polytrauma and HS models that more closely mimic battlefield injuries and resuscitation protocols and that IL-6 merits consideration as a resuscitation adjuvant for use by medics at the time of Hextend administration to soldiers suffering from T-HS.

We outlined five highly focused Specific Aims to examine this hypothesis:

Aims 1, 2, and 3. To determine the effects of IL-6 administration at the start of resuscitation on survival, vital organ apoptosis, injury, inflammation and mitochondrial dysfunction in two rodent models and one swine model that mimic combat casualties and current battlefield fluid resuscitation strategies (Hextend infusion, 14.3 ml/kg):

1) Rats subjected to laparotomy and controlled HS (AIM 1),
2) Rats subjected to femur fracture and T-HS (AIM 2) and
3) Swine subjected to laparotomy, splenectomy, tissue injury and controlled HS (AIM 3).

Aim 4. To determine the effects of IL-6 administration on the transcriptome induced by these T-HS models in rats and swine.

Aim 5. To determine if leukocyte apoptosis can serve as a biomarker of vital organ apoptosis and injury in T-HS patients.

These studies will establish whether or not the benefits of IL-6 administration will extend to battlefield resuscitation protocols for controlled HS in the setting of moderate to severe trauma and will establish the foundation for clinical trials of IL-6 in civilian injuries involving trauma and HS that mimic severe combat injuries.

BODY:

In our original Statement of Work document, we delineated that Tasks in Aims 1, 2, 4 and 5 would be performed in Year 1 and 2 as summarized in the Gantt chart below:

TIMELINE (GANTT CHART)

	YEAR 1	**YEAR 2**	**YEAR 3**
Specific Aim 1. Effects of IL-6 in rat Lap/HS model			
	Tasks 1A, B, C and D		
Specific Aim 2. Effects of IL-6 in rat FFx/HS model			
		Tasks 2A, B, C and D	
Specific Aim 4. Effects of IL-6 on rat and swine organ apoptosis and inflammation transcriptomes			
		Task 4A	Task 4B / Task 4C
Specific Aim 5. Leukocytes as a marker of organ apoptosis in T-HS patients			
	Tasks 5A, B, C and D		

These Tasks and the progress we have made in each are outlined below.

<u>Specific Aim 1</u>. Determine the effects of IL-6 on survival, organ apoptosis, injury and inflammation and mitochondrial dysfunction in rats subjected to Lap/HS model (timeframe: 18 months)

<u>Task 1A</u>. Optimize "shock load" for Lap/HS model.

<u>Subtask IA1</u>. Amend animal approval to include swine (timeframe=1 month)

This was postponed.

<u>Subtask IA2</u>. Determine survival rate of rats subjected to Lap/HS protocol with shock load=60 min (or appropriate; 10 rats; timeframe 1 month).

In earlier studies performed as part of preliminary studies for this award, we determined that the "shock" load necessary to achieve the target mortality of 50% in the first of our proposed new rat T/HS protocols was 60 min at 35 mm Hg. This protocol includes laparotomy followed by fixed pressure hemorrhagic shock (Rat Lap/HS model). In repeat experiments, we started with a 15-minute period to achieve target MAP of 35 mm Hg followed by 60 min at target MAP. Since there were no deaths, we proceeded to increase the duration of time at target MAP to 75 min, then 90, 120, and 150 and finally 180 min. It was not until using a "shock" load of 150 – 180 min that 50-70% mortality at 48 hr was observed in a total of 6-10 rats examined. Thus, we have identified a shock load that will allow us to assess if use of IL-6 as a resuscitation adjuvant provides a survival benefit, as outlined below.

While optimizing the "shock load" for the Rat Lap/HS model, we completed rat studies for a critical experiment at the request of our industry partner (Novartis). Novartis is convinced that prevention of kidney injury is the most compelling pathway for entry into clinical use of human recombinant IL-6 as a resuscitation adjuvant. They have developed a panel of sensitive urine analyte assays to test for kidney injury, which they wanted to use to establish if kidney injury occurred in our standard rat T/HS model and to determine whether kidney injury could be prevented by use of IL-6 as a resuscitation adjuvant. In this experiment, we subjected 6 rats each to either our sham protocol or our standard T/HS protocol, as described (1-3) modified per this grant proposal. Specifically, rats were subjected to trauma (groin incision and bilateral superficial femoral artery cannulation) followed by hemorrhagic shock. Instead of being resuscitated with heparinized shed blood and lactated Ringer's solution, they were resuscitated with Hextend as described in this proposal combined with IL-6 as a resuscitation adjuvant at four doses (0, 3, 10 or 30 mg/kg). Serum was harvested at 24 and 48 hrs; urine was harvested at 4, 12, 18, 24, 36, 42 and 48 hr; and kidneys were harvested at 48. Samples of serum and urine were sent to Novartis on February 23 to be examined in their kidney injury panel. These studies were intended to answer several important questions: 1) Does kidney injury accompany heart, lung and liver injury in rat T/HS? 2) What is the most sensitive and robust urine test to monitor for kidney injury in this setting? 3) Can IL-6 prevent T/HS-induced kidney injury? 4) If so, what is the optimum dose of IL-6 to use in the rat T/HS studies outlined in our proposal?

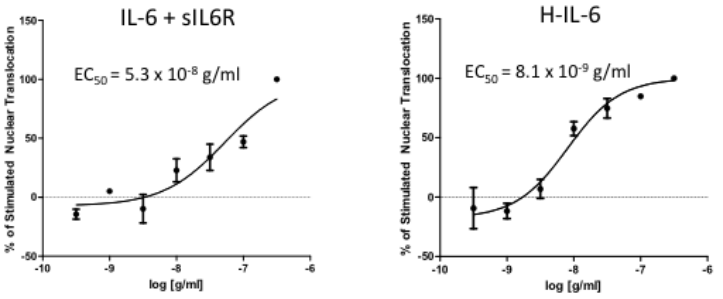

Figure 1. Percent of maximum stimulated nuclear translocation of GFP-Stat3 in murine fibroblast cell expressing GFP-Stat3. Assay performed as described (1) with increasing concentrations of IL-6 and sIL-6R (left panel) or H-IL-6 (right panel).

We received the results from Novartis on August 2, 2011. Of the 10 urine markers of kidney injury, 7 demonstrated evidence of substantial increase including GSTYb, NGAL, Kim-1, Cystatin, beta2M, albumin, and clusterin, which indicated that the kidney demonstrated clear evidence of injury in this model of T/HS. Evidence of injury was maximal by 4 hours. The most sensitive and robust urine marker of kidney injury was Kim-1, but most of the 7 indices were nearly equally sensitive. Somewhat to our surprise, however, while there was some suggestion of protection by IL-6 against renal injury determined by Kim-1 and albumin levels at an IL-6 dose of 10 ug/kg, these results were not statistically significant. Neither was there evidence of benefit of IL-6 on liver and heart injury. The inability to demonstrate a clear benefit of IL-6 at any of the three doses was at odds with all of our earlier publications (1-5). Two major hypotheses for this disparity are: 1) the ability of Hextend to adsorb either IL-6 or sIL-6R, and 2) the absence within the

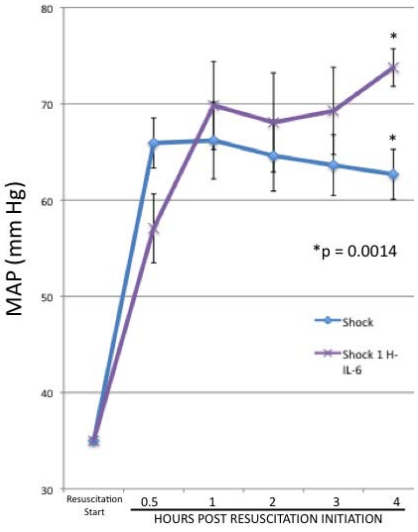

Figure 2. Resuscitation with Hextend + hyper (H) IL-6 improves 4-hr post-resuscitation MAP.

Hextend of a factor(s) present within the returned shed blood (previously used for resuscitation) that are necessary for the beneficial effect of IL-6. The leading candidate for this "missing factor" was sIL-6R.

To explore the hypothesis that Hextend adsorbs either IL-6 or sIL-6R thereby blunting its effects, we examined whether Hextend interferes with the ability of IL-6 alone or in combination with sIL-6R to induce nuclear translocation of GFP-Stat3 in a high-throughput fluorescence microscopy assay we developed to identify small-molecule Stat3 inhibitors (1). The results of this study indicated that Hextend had no effect on the potency of either IL-6 or sIL-6R.

To explore the hypothesis that shed blood but not Hextend contains a factor(s) such as sIL-6R necessary to realize the beneficial effects of IL-6, in the fourth quarter, we examined the collected shed blood for the presence of sIL-6R as a function of time of accumulation in our standard T/HS protocol. Our results demonstrated that shred blood accumulated sIL-6R over time to concentrations (100 ng/ml) equivalent to those of recombinant hIL-6 expected within the circulation of rats receiving the 3 ug/kg dose, the dose we initially reported to be of benefit (2).

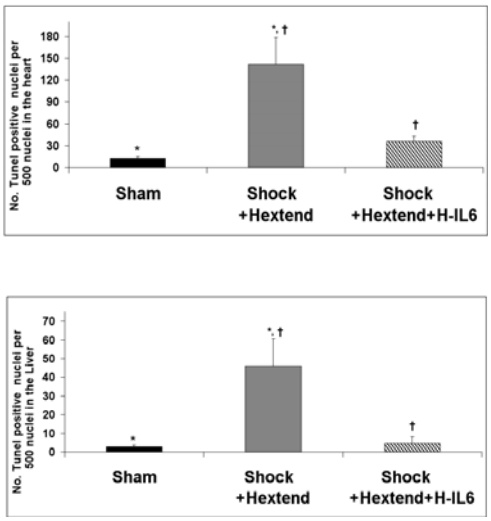

Figure 3. Hyper (H) IL-6 prevents T/HS-induced cardiomyocyte (top panel) and hepatocyte (bottom panel) TUNEL-positivity. Comparisons marked by * or †, $p < 0.02$).

This finding strongly suggested that the heparinized shed blood was contributing a factor, most likely sIL-6R, that was facilitating the effect of IL-6 and that this factor was absent in Hextend. We designed an experiment consisting of 7 groups of rats @4 rats/group to test this hypothesis:

- **Group 1:** Sham
- **Group 2:** Shock with Hextend resuscitation
- **Group 3:** Shock with IL-6 @ 10 μg/kg with Hextend resuscitation
- **Group 4:** Shock with IL-6 and sIL-6Rα both @ 10 μg/kg with Hextend resuscitation
- **Group 5:** Shock with IL-6 @ 10 μg/kg, shed blood bolus, and 2X total shed blood volume of Ringer's lactated saline (our established resuscitation protocol)
- **Group 6:** Shock with hyper (H)-IL-6 @ 10 μg/kg with Hextend resuscitation
- **Group 7:** Shock with H-IL-6 @ 1 μg/kg with Hextend resuscitation

Groups 6 and 7 will test the sub-hypothesis that H-IL-6, a chimeric protein consisting of human IL-6 fused to the human soluble IL-6 receptor (sIL-6R) α, will be even more potent that the combination of IL-6 and sIL-6Rα. Support for this hypothesis was provided *in vitro* by studies in which we performed a dose-response curve comparing the potency H-IL-6 vs. IL-6/sIL-6Rα (1:1 ratio; **Figure 1**). H-IL-6 was nearly 7-fold more potent that IL-6 + sIL-6R in causing nuclear translocation of GFP-Stat3 in murine embryonic fibroblasts.

Preliminary analysis of the results to date indicates a striking improvement in the post-resuscitation blood pressure for Group 7 vs. Group 2 (**Figure 2**). Also, cardiomyocyte and hepatocyte apoptosis as determined by TUNEL staining was completely prevented in Group 7 vs. Group 2 (**Figure 3**). In addition, lung, heart and kidney apoptosis induced by T/HS as measured by nucleosome levels was almost completely prevented in Hextend-resuscitated rats that received either a combination of IL-6 + sIL-6R or H-IL-6 (1 or 10 ug) vs. rats that received Hextend alone or Hextend + IL-6 (**Figure 4**).

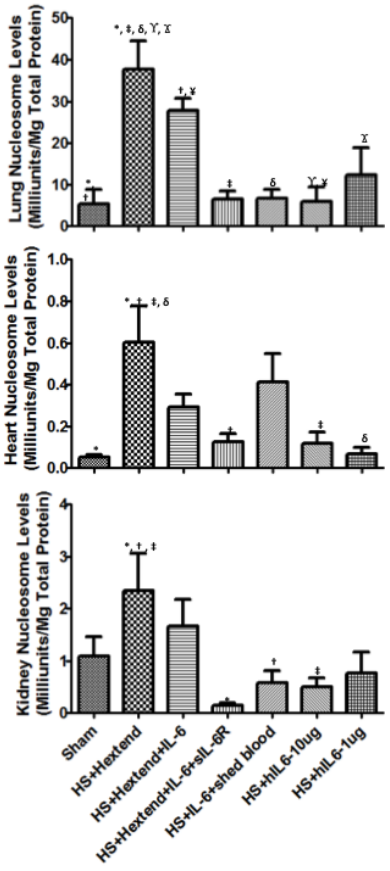

Figure 4. Hyper (H) IL-6 and IL-6 + sIL-6R prevents T/HS-induced lung (top panel), heart (middle panel) and kidney (bottom panel) increase in nucleosomes. Comparisons marked by symbols $p < 0.05$).

To these preliminary but very exciting findings, we have added the findings that the liver IL-6 mRNA levels, which are increased 3-fold by T/HS (Group 2 vs. Group 1), return to normal when H-IL-6 is combined with Hextend (Group 7 vs. Group 2); **Figure 5**). These results continue to support the hypothesis that the

missing factor when Hextend is used as the major resuscitation fluid instead of shed blood is sIL-6R and further suggests that hyper (H) IL-6 is fully capable of replacing IL-6 when Hextend is used as a resuscitation adjuvant instead of heparinized whole blood.

We plan to complete the analysis of all Groups in a focused way as outlined in **Table 1** in the first quarter of Year 3 then return to completing Task 1B, 1C, 1D, 2A, 2B, 2C, and 2D during the remainder of the year. Critical for these studies will be obtaining sufficient quantities of hyper-IL-6 from our colleague (Stefen Rose-John) in Germany or clearly establishing that IL-6 plus sIL-6Rα together work as well as hyper IL-6 alone.

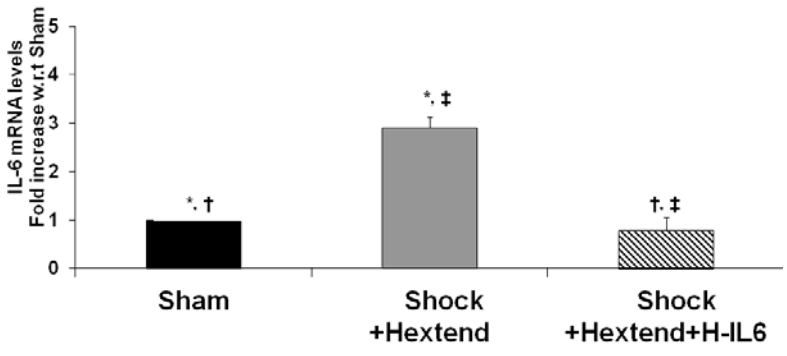

Figure 5. Liver IL-6 mRNA levels in the three groups indicated (n=4 per group). Pairs of bars marked by a symbol (*, etc.) indicate a significant difference ($p<0.05$).

Table 1. Endpoints determinations.

Organ	Endpoints and Assays Used				
	Quantification of Total and p-Stat3	Quantification of inflammatory cytokine production (IL-6)	Quantification of inflammation (neutrophil influx)	Quantification of Apoptosis	
	Luminex bead assay	Real Time RT-PCR	Myeloperoxidase staining	TUNEL assay	Nucleosome ELISA
Liver	Yes	Yes	Yes	Yes	Yes
Lung	Yes	Yes	Yes	Yes	Yes
Heart	Yes	Yes	No	Yes	Yes
Kidney	Yes	Yes	No	Yes	Yes

<u>Task 1B</u>. Determine the effect of IL-6 on survival in the rat Lap/HS model.

<u>Subtask IB1</u>. Randomly assign rats to the Lap/HS/Hex/P or Lap/HS/Hex/IL-6 groups and observe for 72 hr and record mortality. (20 rats; timeframe=2 months)

While the Novartis experiment was being analyzed by the company in Year 1, we proceeded with an IL-6 survival study in the Rat Lap/HS model in which the shock load was 180 min at target MAP of 35 mm Hg. Eighteen rats were entered into this protocol and randomized to receive either IL-6 (10 ug/kg in 0.1 ml PBS) or PBS alone as a resuscitation adjuvant. Randomization was performed in such a way that the animal surgeon was blinded to the resuscitation adjuvant each animal received. The PI broke the code on the randomization after 18 rats had been studied. The results demonstrated that while mortality in the IL-6-treated arm (n=10) was 20%, mortality in the placebo arm was only 25%, lower than the 50% expected.

With the findings above strongly suggestion that H-IL-6 can substitute for IL-6 when Hextend is used as the resuscitation fluid, we have begun a repeat experiment in which 20 rats will be entered into the survival protocol and randomized to receive either H-IL-6 (1 ug/kg in 0.1 ml PBS) or vehicle control (0.1 ml PBS). It will be completed the first quarter of year 3.

<u>Task 1C</u>. Determine the effect of IL-6 on left ventricular contractile function, apoptosis within the heart, lung, liver, kidney, kidney and leukocytes, injury and inflammation within the lung and liver and mitochondrial dysfunction within liver and hearts.

To lay the foundation for the mitochondrial portion of these studies, we performed a preliminary study to evaluate the potential acute effect of IL-6 administration on mitochondrial function. Three pairs of rats were administered either 10 ug/kg IL-6 (ip) or vehicle (PBS) and one hour later the animals were sacrificed, organs (heart, kidney, liver and lung) harvested, and mitochondria were isolated. The isolated mitochondria were assayed for respiration by polarography, for respiratory chain activities by spectrophotometry, and for relative mitochondrial reactive oxygen species (ROS) levels by measuring native and total reduced aconitase activities. The results of studies on mitochondria isolated from each of the four tissues of IL-6 treated animals were unchanged compared to control-treated animals.

During the past year, we have perfected performing mitochondrial respiration analyses on isolated mitochondria from various rodent tissues as well as on mouse embryonic fibroblasts (MEFs). We have optimized the conditions for measuring respiration of mitochondria from rat heart, liver, kidney and lung and are beginning the process of performing respiration analyses of mitochondria from multiple tissues of paired rats subjected to the standard trauma/hemorrhagic shock model with or without IL-6 administration as an adjuvant resuscitative agent. We have also performed cellular respiration studies on MEFs that completely lack Stat3 (Stat3Δ), express only the Stat3 α isoform (Stat3α), express only the Stat3 β isoform (Stat3β), or express only the Stat3 β isoform that has the last 7 amino acids deleted (Stat3βΔ7). Compared to wild type MEFs, Stat3α and Stat3β cells exhibit normal respiration, while Stat3Δ and Stat3βΔ7 MEFs exhibit significant mitochondrial respiration defects. Mitochondrial electron transport chain enzyme studies demonstrate partial complex I and II deficiencies for Stat3Δ and Stat3βΔ7 MEFs compared to wild type, correlating with the observed respirations defects. Interestingly, when pretreated with 200 ng/mL of IL-6 and soluble IL-6 receptor for 1 hour, Stat3Δ MEFs exhibit a significant relative increase in respiration that is not observed in wild type or the other MEFs. These preliminary observations will be followed up during the coming year.

<u>Task 1D</u>. Determine the effect of Stat3 inhibition with the GQ-ODN T40214 on IL-6-mediated prevention of T-HS-induced mortality, left ventricular contractile dysfunction, organ apoptosis, injury and inflammation and mitochondrial dysfunction.

We have developed a better-characterized small-molecule Stat3 inhibitor (1, 7) that we will use instead of GQ-ODN T40214.

Specific Aim 2. To determine the effects of IL-6 administration on survival, vital organ apoptosis, injury and inflammation and mitochondrial dysfunction in rats subjected to FFx/HS model (timeframe: 18 months).

Tasks 2A, B, C, and D will be performed upon completion of Aim 1.

Specific Aim 4. To determine the effects of IL-6 on the T-HS-induced apoptosis and inflammation transcriptome within the heart, lung, liver, kidney and leukocytes of rats and swine subjected to T-HS and resuscitation protocols (timeframe=12 months; in Year 2).

Since submission of the proposal in which we presented preliminary data regarding the effect of our standard T/HS protocol on the liver inflammation transcriptome and its beneficial modulation by IL-6, we have published these findings in *PLoS ONE* (8). In addition, the PI was invited to give a plenary presentation to the 34th Annual Conference on Shock (Norfolk, VA; 06/12/11; "Contributions of Abnormal Proteostasis to Cellular Dysfunction"). This talk and the data presented therein formed the basis for a peer-reviewed manuscript entitled, "Contribution of the Unfolded Protein Response (UPR) to Hepatocyte and Cardiomyocyte Apoptosis and its Prevention in Trauma/Hemorrhagic Shock", provisionally accepted to *Science Reports* (Nature Press) [**Appendix 1**; (9)]. This paper reports the first global transcriptome analysis of the UPR in the liver and heart in T/HS; it strongly implicates the non-canonical UPR proteins, heat shock proteins (Hsp) 70 and Hsp40, as modulating hepatocyte apoptosis and mediating protection against apoptosis in response to IL-6. This finding opens new avenues for intervention in the prevention of apoptosis in this setting such as proteostasis modulators. In addition, Stephen Thacker, a talented post-doctoral fellow in the laboratory and first author of this submission, has submitted 4 abstracts in the last year to annual national meetings of the Shock Society, the Infectious Diseases Society of America, the Pediatric Academic Society, and the Pediatric Infectious Diseases Society (**Appendix 2**) describing the UPR and it role in alveolar epithelial cell apoptosis in T/HS and its prevention by IL-6.

<u>Specific Aim 5</u>. To determine if circulating leukocytes can serve as a marker for T-HS-induced apoptosis in T-HS patients (timeframe=16 months).

<u>Task 5A</u>. Amend IRB protocol (timeframe=4 months).

This Task was accomplished.

<u>Task 5B</u>. Isolate peripheral blood leukocytes from T-HS patients upon entry into the standard vs. hypotensive resuscitation protocol study at the time of randomization (time 0) and at 60-minute intervals until the end of surgery then 1 after the end of surgery and 24 hr after randomization (17 patients; timeframe=10 months).

This Task was accomplished; see below.

<u>Task 5C</u>. Perform nucleosome ELISA on leukocyte extracts (timeframe=1 month).

This Task was accomplished; see below.

<u>Task 5D</u>. Perform TUNEL of leukocytes (timeframe=1 month).

Tasks 5B, 5C and 5C were accomplished with the following modifications. Instead of studying only 17 patients, we examined 41 patients. Also, rather than isolating WBC for ELISA and TUNEL at the time of randomization, every hour after randomization, 1 hour after the end of surgery and 24 hours after randomization, we opted to drop the hourly examinations during surgery because of the difficulty in coordinating blood sampling while the patient was undergoing life-saving surgery. Instead, we collected blood for WBC isolation and examinations at the time of randomization, 1 hour after the end of surgery and 24 hour after randomization. Our results demonstrated that there was very little difference in leukocyte apoptosis or any other clinically relevant parameter between these two groups. Consequently, the two group were pooled resulting in the finding [**Appendix 3**; (10)] that the circulating leukocytes of T/HS subjects who survived to hospital discharge without developing any infections had significantly higher nucleosome levels 1-hr post-operative compared to those who did develop an infection (49.8 mU/mg protein versus 19.8 mU/mg protein, p=0.02). This difference persisted when analyzing by specific type of infection. TUNEL staining revealed that 72% of apoptotic cells were PMNs. There were no statistically significant correlations between nucleosome levels and survival. Thus, our results indicated that in patients with hemorrhagic shock, increased peripheral blood PMN apoptosis is associated with reduced risk of developing subsequent infection. Previous research has shown that high levels of apoptosis in circulating neutrophils following shock may have a protective effect by preventing neutrophil infiltration and limiting release of harmful oxygen radicals in the tissues. Thus, neutrophil apoptosis may render tissues less susceptible to injury and subsequent infection consistent with strategies aimed at benefiting this patient population by limiting PMN number and aberrant function early in the resuscitation period.

As noted, our results did not demonstrate an association between leukocyte apoptosis and survival. Consequently, leukocyte apoptosis cannot serve as a robust biomarker for predicting patients who may benefit from IL-6 as a resuscitation adjuvant. Given the results above demonstrating the sensitivity of urinary injury biomarkers in our rat T/HS model, we have begun to collect the urine of T/HS patients for measurement of markers of renal injury to establish the best biomarker of renal injury in this patient population to replace leukocyte apoptosis for this purpose. Urine will be collected at the same time points as previously used for blood plus 7 days after randomization.

Thus, all of Aim 5 has been accomplished resulting in a published manuscript (10). We have made good progress in Aim 1. It along with Aim 2 will be rapidly completed now that we have established the requirement for sIL-6R to achieve benefit from IL-6 when Hextend is used for resuscitation.

KEY RESEARCH ACCOMPLISHMENTS:

- We demonstrated that kidney injury and apoptosis accompanies heart, lung and liver injury and apoptosis in rat T/HS. Similar to apoptosis in these other organs, kidney apoptosis is prevented when IL-6 is used a resuscitation adjuvant with heparinized shed blood (**Figure 4**, bottom panel).
- Kidney injury was readily detected within the urine 4 hours after the initiating of resuscitation using 7 of 11 analytes tested by Novartis; 4 of these 7 analytes are available for purchase and use in a Luminex bead-based assay system in the Tweardy lab.
- Results demonstrated that heparinized shed blood accumulated sIL-6R over time to concentrations equivalent to those of recombinant hIL-6 expected within the circulation of rats receiving the 3 ug/kg dose, the dose we initially reported to be of benefit (2).
- Recent results have determined that sIL-6R is an essential factor, in addition to IL-6, for prevention of apoptosis when IL-6 is used as a resuscitation adjuvant in combination with Hextend.
- Leukocyte apoptosis appears not to be sufficiently robust enough biomarker for predicting mortality in T/HS patients.
- However our circulating neutrophil (PMN) apoptosis results indicated that in patients with hemorrhagic shock, increased peripheral blood PMN apoptosis is associated with reduced risk of developing subsequent infection.
- In the first global analysis of the UPR transcriptome ever performed, we identified two non-canonical UPR modulators, Hsp70 and Hsp40, as potential key modulators of liver and lung apoptosis in T/HS that mediate the beneficial effects of IL-6.

REPORTABLE OUTCOMES:

Manuscripts:

1. Morrison, C.A., Moran, A., Huby M.P., Tweardy, D.J., and Carrick, M.M. 2011. Increased Apoptosis of Peripheral Blood Neutrophils is Associated with Reduced Risk of Infection in Trauma Patients with Hemorrhagic Shock. J Infect. 2013 Jan;66(1):87-94. doi: 10.1016/j.jinf.2012.10.001. Epub 2012 Oct 9. PMID: 23063873.
2. Thacker, S.A., and Tweardy, D.J. 2011. Contribution of the Unfolded Protein Response to Hepatocyte and Cardiomyocyte Apoptosis and its Prevention in Trauma/Hemorrhagic Shock. *Science Reports* (Nature Press), provisionally accepted for publication.

Abstracts:

1. Thacker SA, Moran A, Huby M and Tweardy DJ. Contribution of Heat Shock Proteins 70 and 40 to Prevention of Alveolar Epithelial Cell Apoptosis in Trauma Complicated by Hemorrhagic Shock. Submitted to the Annual Meeting of the Pediatric Academic Society 2012.
2. Thacker SA, Moran A, Huby M and Tweardy DJ. Contribution of the Unfolded Protein Response to Prevention of Alveolar Epithelial Cell Apoptosis in Trauma Complicated by Hemorrhagic Shock. Submitted to the Annual Meeting of the Pediatric Infectious Diseases Society 2012.
3. Thacker SA, Moran A, Tweardy DJ. Impact of Trauma/Hemorrhagic Shock on the Unfolded Protein Response Transcriptome of the Heart, Lung, and Liver. June 2012 International Federation of Shock Societies Meeting Miami, FL.
4. Thacker SA, Moran A, Huby P, Tweardy DJ. Impaired Host Defense of the Lung Following Trauma with Hemorrhagic Shock: Implicating the Unfolded Protein Response in Alveolar Epithelial Cell Apoptosis. Annual Meeting of the Infectious Diseases Society of American/ID Week, October 2012.

National Presentations:

Oral:

1. Stephen Thacker, Ana Moran, David Tweardy. Implicating the Unfolded Protein Response in Impaired Innate Immunity of the Lung Following Trauma with Hemorrhagic Shock. IDWeek October 2012, San Diego, CA. Oral Presentation.
2. Stephen Thacker, Ana Moran, David Tweardy. Contribution of the Unfolded Protein Response to Prevention of Alveolar Epithelial Cell Apoptosis in Trauma Complicated by Hemorrhagic Shock. April 2012 Pediatric Academic Societies (PAS) Boston, MA. Oral Platform Presentation.

Poster:

3. Stephen Thacker, Ana Moran, David Tweardy. Impact of Trauma/Hemorrhagic Shock on the Unfolded Protein Response Transcriptome of the Heart, Lung, and Liver. June 2012 International Federation of Shock Societies Meeting Miami, FL. Poster Presentation.
4. Stephen Thacker, Ana Moran, David Tweardy. Contribution of the Unfolded Protein Response to Prevention of Alveolar Epithelial Cell Apoptosis in Trauma Complicated by Hemorrhagic Shock. 2012 St. Jude/PIDS Research Conference, Memphis, TN, February 2012. Poster Presentation.

CONCLUSIONS:

We have performed a global transcriptome analysis of the UPR in the liver and heart in T/HS that strongly implicates Hsp70 and Hsp40 as modulating hepatocyte apoptosis and mediating protection against apoptosis in response to IL-6. This finding opens new avenues for intervention in the prevention of apoptosis in this setting such as proteostasis modulators.

We demonstrated in patients with hemorrhagic shock that increased peripheral blood PMN apoptosis is associated with reduced risk of developing subsequent infection. Previous research has shown that high levels of apoptosis in circulating neutrophils following shock may have a protective effect by preventing neutrophil infiltration and limiting release of harmful oxygen radicals in the tissues. Thus, neutrophil apoptosis may render tissues less susceptible to injury and subsequent infection consistent with strategies aimed at benefiting this patient population by limiting PMN number and aberrant function early in the resuscitation period.

Our findings demonstrate that sIL-6R is an essential factor, in addition to IL-6, for prevention of apoptosis when IL-6 is used as a resuscitation adjuvant in combination with Hextend. This requirement can be met by either adding sIL-6R to the IL-6 for use as a resuscitation adjuvant or substituting hyper (H) IL-6 for IL-6 when Hextend is used as the resuscitation fluid. We are pursuing efforts to collaborate with Stefan Rose-John to commercialize H IL-6 for this purpose.

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APPENDICES:

Appendix 1: Thacker et al manuscript provisionally accepted by *Science Reports* (Nature Press).

Appendix 2: Thacker et al abstracts for annual meetings of IDSA, PAS, PIDS and SHOCK Society

Appendix 3: Morrison et al manuscript published in *J Infection.*

Cover Page

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MODULATION OF THE UNFOLDED PROTEIN RESPONSE DURING HEPATOCYTE AND CARDIOMYOCYTE APOPTOSIS IN TRAUMA/HEMORRHAGIC SHOCK

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ABSTRACT

Trauma with hemorrhagic shock (T/HS), has been shown to result in liver injury marked by hepatocyte apoptosis and heart failure marked by cardiomyocyte apoptosis, both of which we have shown to be prevented by IL-6 administration at resuscitation, and Stat3 largely mediated this. As specific mediators have not been delineated, we investigated the unfolded protein response (UPR), which, with marked activation, can lead to apoptosis. Prior studies of hepatic and cardiac injury examined limited repertoires of UPR elements, making it difficult to assess the role of the UPR in T/HS. This study describes the first global examination of the UPR transcriptome in the liver and heart following T/HS, demonstrating organ-specific UPR transcriptome changes. The non-canonical UPR chaperone, Hsp70, was most dysregulated following T/HS and may contribute to hepatocyte protection via an IL-6-mediated pathway, identifying a potential new therapeutic strategy to prevent hepatocyte death and organ dysfunction in T/HS.

INTRODUCTION

Trauma is a leading cause of morbidity and mortality in the United States for those under the age of 45 years, especially when complicated by hemorrhagic shock [1]. When trauma with hemorrhagic shock (T/HS) is accompanied with resuscitation, the end effect is essentially a systemic ischemia and reperfusion injury. Multiple organ failure is an important maladaptive sequelae contributing to late mortality in those who survive beyond 24 hrs following severe T/HS and resuscitation [2].

Work done by our group, and others, in rodent models of T/HS, has shown that parenchymal cells within organs such as the liver, a key metabolic and homeostatic organ, and heart, an organ whose dysfunction often heralds post-traumatic mortality, undergo apoptosis [3-7]. The pathways leading to parenchymal cell apoptosis in these organs in T/HS are not fully understood. The classical mechanisms of apoptosis, such as the extrinsic and intrinsic apoptotic pathways, have been investigated in the liver and heart [3,6]. However, specific delineation of the pathways leading from T/HS to cell death and organ dysfunction is incomplete.

Prolonged or severe endoplasmic reticulum (ER) stress has recently been demonstrated to lead to apoptosis through the unfolded protein response (UPR). The canonical genes involved in ER stress and the UPR were first delineated in yeast including identification of the ER membrane bound sensors of ER stress [8-11]. Homologues for these sensors and their targets have been identified in mammals and their activation can reliably be assessed transcriptionally. While much of the focus of

investigation on the UPR has centered around the three main signaling molecules inositol-requiring enzyme 1α (IRE1α), Activating Transcription Factor 4 (ATF4), and protein kinase RNA-like endoplasmic reticulum kinase (PERK), many non-canonical modulators of the UPR have been identified linking the UPR to pathways ranging from innate immunity to apoptosis. Emerging evidence has shown that prolonged ER stress and UPR activation leads to apoptosis that is an important mechanism of disease pathogenesis in a number of genetic disorders, such as lysosomal storage diseases, particularly within the liver [12,13]. Examination of the UPR as a potential cause of parenchymal cell apoptosis in metabolic and other derangements leading to ER stress initially focused on exocrine organs such as the liver [14]. The UPR and its contribution to liver disease has been investigated in liver diseases such as steatosis [15,16], ischemia/reperfusion injury [17,18] and T/HS [19,20]. The impact of the ER stress and the UPR on non-exocrine organs such as the heart, has only recently become a focus [21,22]. Studies of both the liver and heart are limited, however, since they have focused on isolated components of the UPR and did not provide direct evidence that would allow one to conclude that apoptosis or organ injury resulted from an insufficient adaptive UPR or that the UPR or components therein were, in fact, maladaptive.

We previously demonstrated that parenchymal cell apoptosis following T/HS in both the liver and heart is prevented by administration of IL-6, which mediates its effect through the actions of Stat3 [3,6]. In the current studies, we performed UPR transcriptome analysis of the liver and heart at a global level to identify candidate genes within the canonical and non-canonical UPR that contribute to apoptosis following T/HS. By

tracking the direction and magnitude of changes in levels of these candidate genes that occurred following T/HS with IL-6 resuscitation, with or without Stat3 inhibition, we were able to clearly identify those genes most implicated in T/HS-induced apoptosis and its prevention by IL-6-activated Stat3. In particular, we demonstrated that Hsp70 and 40 were upregulated in the liver by T/HS, and that this response was adaptive and insufficient since IL-6 augmented it, thereby preventing apoptosis.

METHODS

Rat T/HS protocol. For the rat experiments in this study, 8-week old male Sprague-Dawley rats (200-250 gm) were used. Rats were subjected to the sham or T/HS protocols, as described [3,6,23] with modifications. Blood was withdrawn into a heparinized syringe to achieve and then maintain the target MAP at 35 mmHg until blood pressure compensation failed. Blood was then returned as needed to maintain the target MAP. The amount of shed blood returned (SBR) defined shock severity as reflected in the duration of hypotension, and the animals used in this analysis received 50% SBR (SBR50; duration of hypotension, 273 ± 24.9 minutes). At the end of the hypotensive period, rats were resuscitated as described [3,6,23] and humanely sacrificed 60 minutes after the start of resuscitation in order to capture the first wave of transcriptional changes. Where indicated, rats received 10 μg/kg of recombinant human IL-6 in 0.1 ml PBS at the initiation of the resuscitation or PBS alone. Sham rats were anesthetized and cannulated for 250 minutes but were not subjected to hemorrhage or resuscitation. Rat livers and hearts were harvested immediately after sacrifice and snap frozen in liquid nitrogen for nucleosome and RNA extraction steps.

In vivo pharmacological inhibition of Stat3. To achieve pharmacological inhibition of Stat3 activity within the rats, the G-rich, quartet-forming oligodeoxynucleotides (GQ-ODN), T40214[24] (2.5 mg ODN/kg) was given by tail vein injection, 24 hours prior to subjecting them to the SBR50 protocol with IL-6 treatment. The half-life of T40214 in tissues is ≥ 48 hours [25].

Nucleosome ELISA. Levels of histone-associated DNA fragments (nucleosomes) were determined in homogenates of snap-frozen liver using an ELISA method (Cell Death

Detection ELISA^{plus}; Roche Diagnostics, Manheim, Germany), as described [6, 23]. The nucleosome concentration for each liver sample was normalized for total protein concentration determined by Bradford assay (Bio-Rad Protein Assay, Bio-Rad Laboratories, Inc., Hercules, CA). The final nucleosome concentration for each liver sample was the average of duplicate determinations.

Terminal deoxynucleotidyl transferase mediated dUTP nick end labeling (TUNEL) staining. TUNEL staining to enzymatically detect the free 3'-OH DNA termini was performed using the ApopTag Plus Peroxidase in situ Apoptosis Detection Kit from Chemicon International (now Millipore, Billerica, MA). Slides were rehydrated from xylene to PBS through a series of decreasing concentrations of ethanol and digested in proteinase K (20 μg/ml) for 3 minutes at 23°C. Endogenous peroxidases were quenched for 30 minutes in 3% hydrogen peroxide in PBS. TdT enzyme was diluted in TUNEL solution buffer then used as suggested by the manufacturer. Slides were counterstained with hematoxyllin. TUNEL positive cells were assessed microscopically by counting the total nuclei and the number of TUNEL-positive nuclei in twenty random 1000x fields by an experienced histologist, blinded to the treatment each rat received. Data is presented as the number of TUNEL positive cells per high power field (hpf).

RNA isolation and oligonucleotide microarray hybridization. Total RNA was isolated from 4-5 micron cryotome sections of liver using TRIzol® Reagent (Invitrogen, Carlsbad, California) single step RNA isolation protocol followed by purification with RNeasy® Mini Kit (QIAGEN, Hilden, Germany) as instructed by the manufacturer. Gene

expression profiling was performed with the Affymetrix Rat Array RAE 230A chips following Affymetrix protocols used within the Baylor College of Medicine Microarray Core Facility.

Microarray Analysis. We used GenespringGX (Agilent Technologies Inc, Santa Clara CA) software package for quality assessment, statistical analysis and annotation. Low-level analyses included background correction, quartile normalization and expression estimation using RMA-based analysis within Genespring. One-way analysis of variance (ANOVA) with contrasts was used for group comparisons on all genes and on the list of UPR entities. P-values were adjusted for multiple comparisons using the Benjamini-Hockberg method. The adjusted p-values represent false discovery rates (FDR) and are estimates of the proportion of "significant" genes that are false or spurious "discoveries". We used a FDR=5% as cut-off. The genechip used, RAE 230A, contained 15,923 probe sets representing 13,521 annotated genes or expressed sequence tags. A UPR gene entity list was created using both Ingenuity Pathway Analysis (IPA® Redwood City, CA) and the Gene Ontology Database©, with keywords "endoplasmic reticulum stress, unfolded protein response". Three or more chips for each organ were hybridized using mRNA isolated from hearts and livers, respectively for each group comparison: Sham (4), T/HS-PBS (4) and T/HS-IL6 (4) and T/HS-IL6-GQ (3) groups.

Quantitative (Q) RT-PCR. Two-step Q-RT-PCR was performed using the ABI Prism 7700 sequence detection system (Perkin-Elmer/Applied Biosystems, Foster City, CA) as described previously [3,26]. Briefly, total RNA (1 μg) was reverse transcribed using

reverse transcription reagents (BioRad catalog no. 170-8842; Hercules, CA); 20% of each RT reaction was used in duplicate PCR reactions using TaqMan® Universal Master Mix II, with uracil N-glycosylase (PN 4440038) and specific primer and probe sets designed by the manufacturer (TaqMan Gene Expression Assay, Applied Biosystems, Darmstadt, Germany)—Hsp70 (Hspa1a; catalog no. Rn04224718_u1), Hsp40 (Dnajb1; catalog no. Rn 01426952_g1), and 18S rRNA (catalog no.Rn03928990_g1). Each PCR amplification run consisted of incubation for 5 min at 95°C, followed by 40 cycles at 95°C for 15 s and 60°C for 1 min. The cycle threshold of each duplicate determination was normalized by subtraction of the cycle threshold for its corresponding 18S rRNA (ΔC_T). Each ΔC_T was then calibrated by subtracting the ΔC_T value for control rat tissue ($\Delta\Delta C_T$). RNA amount was expressed as relative units calculated as $2^{-\Delta\Delta CT}$, as described [26].

Statistical Analysis. Statistical differences between experimental groups were analyzed using one-way ANOVA and post-hoc analysis was performed using Student-Newman-Keuls test. T-test analysis performed using unpaired Student's T-test.

RESULTS

T/HS-induced hepatocyte apoptosis is prevented by IL-6 resuscitation; the IL-6 effect is mediated, in part, by Stat3

To confirm our previous findings that T/HS induces liver apoptosis, we measured histone-associated DNA fragments (nucleosomes) in the livers of rats subjected to our T/HS protocol. Nucleosome levels were 13.5 times higher than sham ($p<0.001$, ANOVA; Table 1). The nucleosome results were confirmed by TUNEL staining (Table 1), which also demonstrated that hepatocytes represented the overwhelming majority of cells undergoing apoptosis (data not shown).

Nucleosome levels in the IL-6-resuscitated rats were decreased 7.1 times compared to those of the T/HS group ($p<0.001$) and were similar to sham levels (Table 1). TUNEL staining confirmed these results (Table 1). The number of TUNEL-positive nuclei/hpf in the IL-6 group was decreased 14.2 times compared to the placebo group ($p<0.001$), to levels statistically similar to those of the sham group (Table 1).

Pretreatment of rats with the G-rich, quartet-forming oligonucleotide Stat3 inhibitor (T40214) was accompanied by a return of nucleosomes to levels similar to those of the placebo treated group and 5.9 fold higher that those of the IL-6 treated group ($p<0.001$; Table 1). Similarly, the number of TUNEL-positive nuclei/hpf in livers of rats from the T/HS-IL6-GQ group was 6 fold higher than that of the T/HS-IL6-treated group ($p<0.0001$); Table 1). Nucleosome levels and number of TUNEL-positive nuclei/hpf in livers of rats pre-treated with a NS-ODN before T/HS and IL-6 resuscitation were

indistinguishable from those of the IL-6 group (data not shown). Thus, pharmacological inhibition of Stat3 using T40214 in rats subjected to severe HS resuscitated with IL-6 completely blocked IL-6-mediated prevention of liver apoptosis.

Liver UPR transcriptome is significantly altered in T/HS

We investigated the impact of T/HS on the ER stress response at the transcriptome level, and then defined the role of this ER stress response on the observed reversible hepatic apoptosis. Unbiased hierarchical clustering of our experimental animals based on intervention group and entity clustering with the UPR transcriptome demonstrated the reproducible nature of the impact of T/HS on the UPR transcriptome (Figure 1). Of the broad 185-gene UPR-associated entity list generated via literature review and Ingenuity Pathway Analysis (IPA®), 113 distinct gene entities were annotated and expressed across our chips after spot duplicates were removed. Using this list of 113 genes, 63 (56%) were significantly altered in one-way ANOVA ($p < 0.05$) among all three-group comparisons, T/HS vs. Sham, T/HS-IL6 vs. T/HS, and T/HS-IL6-GQ vs. T/HS-IL6. When the impact of T/HS was looked at specifically, 31 (27%) of those gene entities were significantly dysregulated in the T/HS group when compared to sham, with 55% (17 of 31) significantly upregulated and 45% of gene transcripts downregulated. When asking the question of potential mediators of the protective effect of IL-6, 17 entities were significantly altered in both group comparisons. Taking known apoptotic function of these genes into context, we demonstrated that all UPR-associated genes with known potential pro-apoptotic function were upregulated following T/HS and subsequently normalized with IL-6 (Table 2). The most dysregulated genes within this

intergroup comparison were the chaperones, Heat Shock Protein 70 (25.6-fold), and Heat Shock Protein 40 (5.9-fold), the UPR transcription factor ATF4 (3.1-fold), and endoplasmic oxidoreductin-1-like protein (Ero1l) (9.8-fold) suggesting a strong impact on the protein folding mechanics both in the cytoplasm and the endoplasmic reticulum. Indeed, when assessed by Real-Time PCR (RTPCR), Hsp70 and Hsp40 demonstrated significantly increased transcript levels in T/HS animals when compared to Sham, with 5.1 fold (p=0.004) and 3.5 fold (p=0.001) increase, respectively (Figure 2). Likewise confirming the findings of the microarray analysis, Hsp70 and Hsp40 were found to be significantly further increased in animals resuscitated with IL-6 when compared to T/HS animals that did not receive IL-6 at resuscitation with 11.2 fold (p=0.04) and 4.5 fold (p=0.026) increases, respectively (Figure 2.)

To assess which of these dysregulated genes may be impacted via IL-6 through Stat3, we incorporated animals pre-treated with a pharmacologic Stat3 inhibitor (GQ T40214) then resuscitated with IL-6 to animal resuscitated with IL-6 alone. Using this combined intergroup approach, we found 12 gene entities with significant dysregulation across all three-group comparisons (Table 3). Interestingly, we find that of the most dysregulated transcripts, the chaperones Hsp70 and Hsp40 demonstrate upregulation in T/HS. In animals in which hepatocyte apoptosis was prevented by receiving IL-6 at resuscitation, we find that Hsp70 and Hsp40 were further upregulated, suggesting a contribution to prevention of hepatocyte apoptosis. When Stat3 is pharmacologically inhibited, however, we find downregulation of these chaperones, suggesting IL-6 acts to upregulate Hsp70/40 via a Stat3-dependent mechanism not previously described.

T/HS-induced cardiomyocyte apoptosis is prevented by IL-6 resuscitation; the IL-6 effect is mediated, in part, by Stat3

To confirm our previous findings that T/HS induces cardiomyocyte apoptosis, we measured histone-associated DNA fragments (nucleosomes) in the hearts of rats subjected to our T/HS protocol. Nucleosome levels were significantly increased in comparison to sham in T/HS rats ($p<0.01$, ANOVA; Table 1). The nucleosome results were confirmed by TUNEL staining with a 12 fold increase in T/HS rats ($p<0.01$, ANOVA; Table 1), which also demonstrated that cardiomyocytes represented the overwhelming majority of cells undergoing apoptosis (data not shown).

Nucleosome levels in hearts from IL-6 resuscitated rats were reduced by more than 15 fold compared to placebo treated rats undergoing T/HS ($p<0.05$, ANOVA). TUNEL assays of sections of rat hearts confirmed these findings with a similar 1.9-fold reduction ($p<0.05$, ANOVA; Table 1).

Pretreatment of rats with a Stat3 inhibitor was accompanied by a return of nucleosomes to levels similar to those of the placebo treated group. Nucleosome levels in the hearts of T/HS-IL6-GQ rats (Table 1) were increased 6-fold compared to hearts from IL-6 resuscitated rats ($p<0.05$, ANOVA; Table 1). Thus, pharmacological inhibition of Stat3 using T40214 in rats subjected to severe T/HS resuscitated with IL-6 completely blocked IL-6-mediated prevention of cardiomyocyte apoptosis.

Heart UPR transcriptome is significantly altered in T/HS

The results above demonstrate that cardiomyocyte apoptosis caused by T/HS is largely prevented with administration of IL-6 at time of resuscitation (Table 1). We investigated the impact of T/HS on the ER stress response at the transcriptome level, and then defined the role of this ER stress response on the observed reversible cardiomyocyte apoptosis. Using the previously described UPR gene entity list, we found that of the 113 genes present on the chip, 86 (76%) were significantly altered in one-way ANOVA ($p < 0.05$) among all three-group comparisons, T/HS vs. Sham, T/HS-IL6 vs. T/HS, and T/HS-IL6-GQ vs. T/HS-IL6. When the impact of T/HS was looked at specifically, 29 (26%) of those gene entities were significantly dysregulated when compared to sham, with the majority, 79% (23 of 29) significantly upregulated and 6 gene transcripts downregulated. When asking the question of potential mediators of the protective effect of IL-6, 16 entities were significantly altered in both group comparisons (Table 4). The direction of dysregulation induced by T/HS was reversed by IL-6 in all transcripts identified. When taking known apoptotic functions of these genes and the impact of our experimental model into context, we demonstrated that 4 of the 5 genes with known pro-apoptotic function are upregulated following T/HS and subsequently normalized with IL-6 (Table 4). The most dysregulated genes, those genes with > 2 fold change, within this intergroup comparison were the chaperones, Hsp70 (10 fold), Hsp40 (3 fold), and Hsp105 (2.5 fold), and the negative regulator of PERK, phosphoinositide-3-kinase interacting protein 1 (Pik3ip1) (-3.0 fold), suggesting, as in the liver, a strong impact on the protein folding mechanics both in the cytoplasm and the endoplasmic reticulum. In contrast to the liver however, the heat shock protein chaperones, Hsp70 and Hsp40,

were downregulated in the hearts of IL-6-treated animals, indicating they likely are not contributing to the apoptotic protection conferred by IL-6. When adding the comparison of GQ T40214 to IL-6 group, we found 11 gene entities with significant dysregulation across all three group comparisons, and, of those, 8 suggest potential IL-6 mediated effect through Stat3 (Table 5).

DISCUSSION

Our findings provide the first-ever global description of the UPR transcriptome of the heart and liver following T/HS. We demonstrated that T/HS leads to significant cardiomyocyte and hepatocyte apoptosis, which is prevented through the Stat3-dependent actions of IL-6. We examined the UPR transcriptome to identify candidate gene transcripts responsible for T/HS-induced apoptosis. By utilizing an expanded repertoire of UPR members, both canonical and non-canonical, and the reproducible and measurable outcome of IL-6-preventable apoptosis in our model of T/HS, we were able to identify potential UPR modulators that significantly impact T/HS-induced hepatocyte and cardiomyocyte apoptosis.

In the liver, members of the heat shock family of protein folding chaperones, Hsp70 and Hsp40, emerged as significant potential non-canonical UPR modulators of hepatocyte apoptosis in our model of T/HS. This compares with findings in other models of organ injury, such as work done by Wang et al., which demonstrated that Hsp70 and its induction with geranylgeranylacetone (GGA) can protect against primary proximal tubule apoptosis and acute kidney damage in an ischemic injury model [27], and work done by Kuboki et al., which demonstrated in a partial liver I/R model that induction of Hsp70 with sodium arsenite reduced liver injury, as determined by transaminase levels and histology [28]. Besides their role in protein folding in the cytoplasmic space, heat shock proteins have been linked to the canonical UPR pathways of the endoplasmic reticulum. One example is Hsp72, a Hsp 70 family member, which has been shown to interact with the cytosolic domain of IRE1α, enhancing XBP1 splicing, and attenuating

apoptosis *in vitro* [29]. Heat shock protein chaperones have also been shown to prevent CHOP-induced apoptosis through the Hsp70-DnaJ chaperone pair inhibiting translocation of Bax to mitochondria *in vitro* [30].

Our findings provide *in vivo* data linking the heat shock protein family to hepatocyte apoptosis possibly via a Stat3-dependent mechanism in T/HS. These findings are supported by previous work linking IL-6/Stat3 transcriptional regulation of heat shock protein family members[31]. Hsp70 and Hsp40 appear to contribute to an adaptive and protective process in the liver, demonstrating upregulation in T/HS and further upregulation in livers of IL-6-resuscitated animals, correlating with prevention of apoptosis. However, when animals were pretreated with a Stat3 inhibitor that blocked IL-6's prevention of apoptosis, these chaperone transcripts were downregulated. Thus, these findings suggest that IL-6, via a Stat3-dependent pathway, acts to superinduce Hsp70 and 40 transcripts in T/HS. These findings are supported by the work of Masumichi et al [32], which demonstrate that IL-6 is necessary for upregulation of heat shock protein members, including Hsp70/40, in a model of acetaminophen-induced hepatic injury.

Interestingly, the canonical members of the UPR, while altered, were not the most dysregulated transcripts in the liver. CCAAT/-enhancer-binding protein homologous protein (CHOP), PERK, alpha subunit of eukaryotic initiation factor 2 (Eif2α), activating transcription factor 4 (ATF4), and calreticulin were significantly dysregulated (6 to -1.2 fold change) in T/HS (Supplemental Table 1). When considering those entities altered >

2-fold and taking into account known UPR and apoptotic functions of the canonical UPR members, only the transcriptional profile of ATF4 suggested a maladaptive contribution to hepatocyte apoptosis. However, this maladaptive role does not appear to be mediated through Stat3.

The heart demonstrated a distinctly different UPR transcriptional profile in comparison to the liver. When one considers the nature and functions of these organs, this is not unexpected. The liver is the largest glandular mass of tissue in the body and is highly secretory with both exocrine and endocrine function, whereas the heart, with myocyte predominance, is largely non-secretory with maintenance of biophysical function more paramount. The impact of T/HS on the canonical UPR transcriptome was even less in magnitude in the heart than in the liver. Significantly dysregulated canonical UPR transcripts included CHOP, PERK, X-box binding protein 1 (XBP1), Eif2α, and calreticulin (2.5 to -1.2 fold change) with only ATF4 dysregulated by more than 2 fold in response to T/HS (Supplemental Table 2). When taking into account known UPR and apoptotic function, CHOP, XBP1, and GADD34 exhibit transcriptional profiles suggestive of an adaptive role in T/HS-induced cardiomyocyte apoptosis. Given the fold-change was nominal (1.4 to 2-fold) however, further investigation is required to determine their true contribution to T/HS-induced apoptosis.

The protein folding chaperones, Hsp70 and Hsp40, which proved important modulators of apoptosis in the liver, were upregulated in the heart following T/HS, but were downregulated in animals in which IL-6 prevented cardiomyocyte apoptosis, suggesting

these chaperones may play a maladaptive role in T/HS-induced cardiomyocyte apoptosis. The dichotomous nature of these chaperones' roles in the liver and heart in T/HS is supported by work in other models of organ injury. Indeed, previous studies have suggested that Hsp70 family proteins may serve to augment cardiac inflammation and contractile dysfunction [33,34], and its downregulation in IL-6 treated animals would support this hypothesis, as we have previously demonstrated that IL-6 acts to preserve contractile function following T/HS [3]. However, Yao et al., have recently shown that Hsp70 upregulation may contribute to the cardioprotection against ischemia/reperfusion injury observed with lipopolysaccharide (LPS) pretreatment. [35] Thus, the role of Hsp70 in myocardial ischemia/reperfusion injury may be specific to the insult and requires further study to clarify the adaptive versus maladaptive role it may play in ischemia/reperfusion events such as resuscitated hemorrhagic shock.

In addition to providing a global description of the UPR transcriptome of the heart and liver following T/HS, our findings demonstrate that IL-6, when utilized as a resuscitation adjuvant, may augment a physiologic protective role of Hsp70 and Hsp40 via a Stat3-dependent mechanism, thereby protecting against hepatocyte apoptosis. These findings support the concept that modulators of Hsp70 or 40 may offer a therapeutic strategy for prevention of apoptosis and ultimately hepatic dysfunction following T/HS.

Table 1[§]. Impact of T/HS without and with IL-6 on markers of apoptosis in the heart and liver

	Liver		Heart	
Intervention	**Nucleosome**[a]	**TUNEL**[b]	**Nucleosome**[a]	**TUNEL**[b]
Sham	139 ± 67*	0.9 ± 0.4**	0‡	1.3 ± 0.2‡‡
T/HS	1874 ± 127*†	27 ± 3.6**,††	63 ± 8^{Δ,‡}	16.2 ± 2^{ΔΔ,‡‡}
T/HS-IL6	264 ± 36$^{†¥}$	1.9 ± 0.5$^{††,¥¥}$	4 ± 1$^{◊,Δ}$	8.5 ± 0.2$^{◊◊,ΔΔ}$
T/HS-IL6-GQ	1556 ± 241$^{¥}$	12.3 ± 1.1$^{¥¥}$	24 ± 5$^{◊}$	16.5 ± 1$^{◊◊}$

§ *,†,¥,**,††,¥¥,‡,Δ,◊,‡‡,ΔΔ,◊◊ indicate group comparisons with statistical significance of $p<0.05$, one-way ANOVA. (a) Nucleosome data presented as mU/mg total protein. (b) TUNEL data presented as number of TUNEL-positive nuclei per high power field.

Table 2. Liver UPR Transcripts Significantly Altered in Both T/HS vs. Sham and T/HS/IL6 vs. T/HS Comparisons

Gene Symbol	UPR Function	Apoptosis Function	Regulation		Fold Change	
			T/HS vs Sham	T/HS-IL6 vs T/HS	T/HS vs Sham	T/HS-IL6 vs T/HS
Hspa1a/Hspa1b (Hsp70)	Chaperone	Anti	up	up	25.6	5.5
Hspa1b (Hsp70-1b)	Chaperone	Anti	up	up	18.4	5.9
Ero1l	Disulfide Bond Formation	Anti	up	down	9.8	-3.8
Dnajb1 (Hsp40 Subunit b1)	Chaperone	Anti	up	up	5.9	2.7
Atf4	Transcription Factor	Anti/Pro	up	down	3.1	-2.0
Casp3 (caspase 3)	Apoptosis Signalling	Pro	up	down	1.8	-1.7
Eif2s1 (Eif2α)	Protein Translation	Anti	up	down	1.7	-1.6
Sels	Modulation of ATF6	Uknown	up	down	1.5	-1.3
Eif2ak3 (PERK)	UPR Sensory Molecule	Anti/Pro	up	down	1.4	-1.3
Psmb3	Proteasome Degradation	Anti	down	up	-1.2	1.3
Calr (calreticulin)	Chaperone	Anti	down	up	-1.2	1.2
Uba1	Ubiquitination	Anti	down	up	-1.3	1.2
Psme2	Proteasome Degradation	Anti	down	up	-1.3	1.4
Psme1	Proteasome Degradation	Anti	down	up	-1.3	1.2
Dyt1	ATPase	Anti	down	up	-1.4	1.4
Tmbim6 (Bax inhibitor 1)	Apoptosis Signalling	Anti	down	up	-1.5	1.3
Ccnd1	Cell Cycle Signalling	Anti	down	up	-3.4	2.3

Table 3. Liver UPR Transcripts Significantly Altered T/HS vs. Sham, T/HS/IL6 vs. T/HS and T/HS/IL6/GQ Comparisons

Gene Symbol	Regulation			Fold Change		
	T/HS vs Sham	T/HS-IL6 vs T/HS	T/HS-IL6-GQ vs T/HS-IL6	T/HS vs Sham	T/HS-IL6 vs T/HS	T/HS-IL6-GQ vs T/HS-IL6
Hspa1a/Hspa1b (Hsp70)	up	up	down	25.6	5.5	-9.0
Hspa1b (Hsp701b)	up	up	down	18.4	5.9	-10.8
Ero1l	up	down	down	9.8	-3.8	-1.3
Dnajb1 (Hsp40 subunit)	up	up	down	5.9	2.7	-3.4
Casp3 (Caspase 3)	up	down	up	1.8	-1.7	1.4
Sels	up	down	up	1.5	-1.3	1.4
Eif2ak3 (PERK)	up	down	down	1.4	-1.3	-1.3
Psmb3	down	up	up	-1.2	1.3	1.9
Uba1	down	up	up	-1.3	1.2	1.8
Psme2	down	up	up	-1.3	1.4	2.9
Psme1	down	up	up	-1.3	1.2	2.2
Tmbim6 (Bax inhibitor 1)	down	up	down	-1.5	1.3	-1.2

Table 4. Heart UPR Transcripts Significantly Altered in Both T/HS vs. Sham and T/HS/IL6 vs. T/HS Comparisons

Gene Symbol	UPR Function	Apoptosis Function	Regulation		Fold Change	
			T/HS vs Sham	IL6 vs T/HS	T/HS vs Sham	IL6 vs T/HS
Hspa1a/Hspa1b (Hsp70)	Chaperone	Anti	up	down	10	-6.4
Hspa1b (Hsp701b)	Chaperone	Anti	up	down	7.5	-4.9
Cebpb	Transcription factor	Pro	up	down	5.1	-1.7
Dnaja1 (Hsp40 subunit)	Co-chaperone	Anti	up	down	3.1	-2.3
Hsph1 (Hsp105)	Chaperone	Anti	up	down	2.5	-2.1
Dnajb1 (Hsp40 subunit)	Co-chaperone	Anti	up	down	2.2	-2
Nfe2l2	Transcription factor	Anti	up	down	2	-1.4
Ppp1r15a (GADD34)	Transcription factor	Pro	up	down	2	-1.4
Xbp1 (X-box-protein 1)	Transcription factor	Pro	up	down	1.5	-1.2
Tra1 (Hsp90b1)	Chaperone (ERAD)	Anti	up	down	1.4	-1.3
Calr (calreticulin)	Chaperone	Anti	up	down	1.4	-1.3
Ddit3 (CHOP)	Transcription factor	Pro	up	down	1.4	-1.3
Serp1	protects unfolded proteins from ERAD	Anti	up	down	1.3	-1.2
Sp1	Transcription factor	Pro	down	up	-1.2	1.3
Sels	modulates ATF6	Unknown	down	up	-1.5	1.3
Pik3ip1	negative regulator of PERK	Anti	down	up	-3	1.4

Abbreviation: ERAD, endoplasmic reticulum-associated degradation.

Table 5. Heart UPR Transcripts Significantly Altered Across T/HS vs. Sham, T/HS/IL6 vs. T/HS, and T/HS/IL6/GQ vs. T/HS/IL6 Comparisons

Gene Symbol	Regulation			Fold Change		
	T/HS vs Sham	T/HS-IL6 vs T/HS	T/HS-IL6-GQ vs T/HS-IL6	T/HS vs Sham	T/HS-IL6 vs T/HS	T/HS-IL6-GQ vs T/HS-IL6
Dnaja1 (Hsp40 subunit)	up	down	up	3.1	-2.3	2.0
Hsph1 (Hsp105)	up	down	up	2.5	-2.1	1.5
Nfe2l2	up	down	up	2.0	-1.4	2.0
Ppp1r15a (GADD34)	up	down	up	2.0	-1.4	1.4
Xbp1 (X-box-protein 1)	up	down	up	1.5	-1.2	1.8
Tra1	up	down	up	1.4	-1.3	1.2
Calr (calreticulin)	up	down	up	1.4	-1.3	1.4
Ddit3 (CHOP)	up	down	up	1.4	-1.3	5.5
Sp1	down	up	up	-1.2	1.3	1.6
Sels	down	up	up	-1.5	1.3	3.1
Pik3ip1	down	up	up	-3.0	1.4	1.8

Titles and Legends to Figures

Figure 1. Unbiased hierarchical heatmap clustering based on both UPR entity and experimental intervention of animals confined to 113 UPR-associated gene entities on whole liver preparations. Clustering performed using Hierarchical analysis using Euclidean similarity measure, expression data normalized to chip standards for clustering.

Figure 2. Q-RT-PCR using TaqMan® (Life Technologies) for (A) heat shock protein 70 (Hsp70; Hspa1a) and (B) heat shock protein 40 (Hsp40; Dnajb1) performed on whole liver samples from Sham (n=6), trauma with hemorrhagic shock (T/HS, n=4), and T/HS animals resuscitated with IL-6 (T/HS-IL6, n=4). Transcript values reported as relative quantification (RQ) in comparison to a normal rat liver. Values expressed as mean RQ ± SEM. “*”, “**” indicate group comparisons which are statistically different ($p<0.05$) by T-test.

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New figure 1

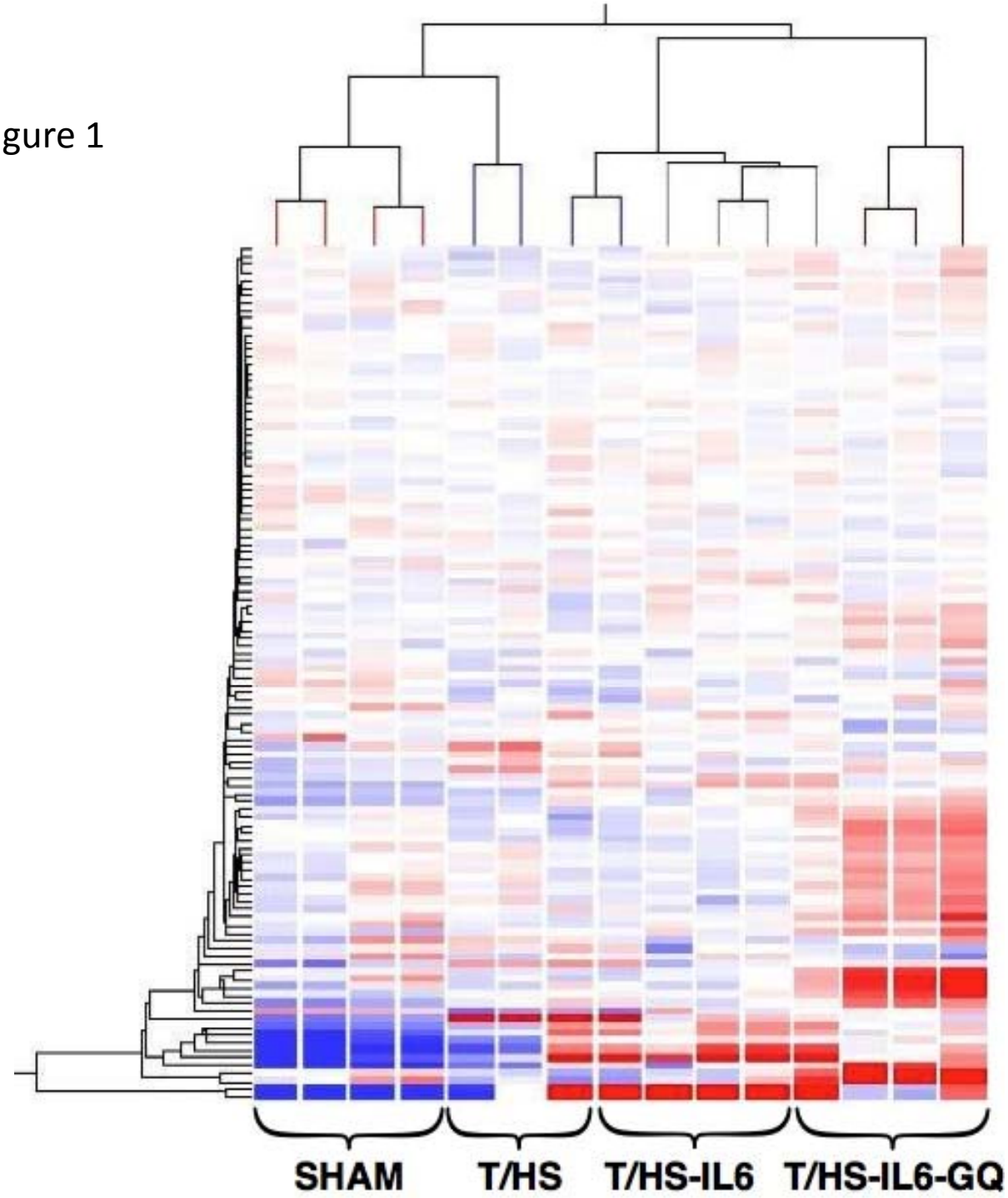
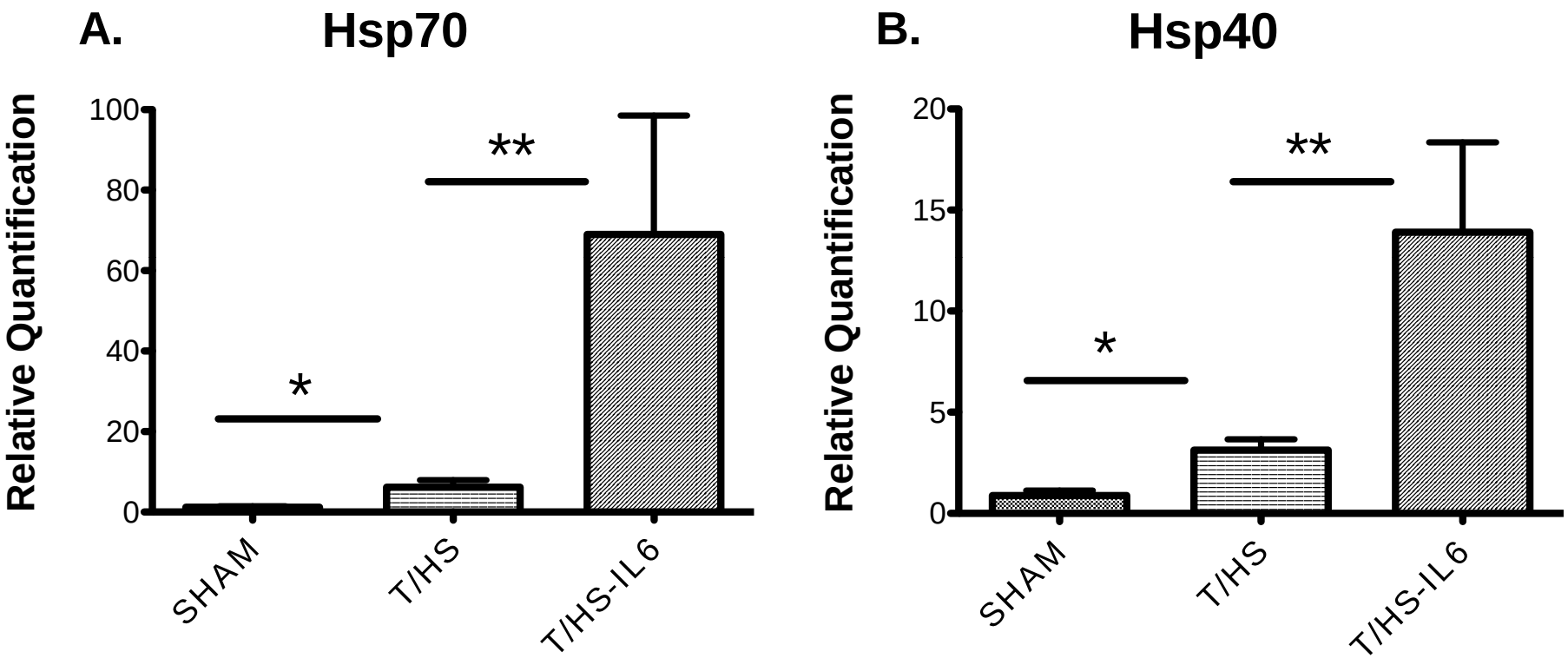


Figure 2, revised



587. Impaired Host Defense of the Lung Following Trauma with Hemorrhagic Shock: Implicating the Unfolded Protein Response in Alveolar Epithelial Cell Apoptosis

Part of Session: 80. Host Response and Pathogenesis 2:15 p.m.

STEPHEN THACKER, MD, ANA MORAN, MD, PILAR HUBY, MD and DAVID J. TWEARDY, MD; Baylor College of Medicine, Houston, TX

Background: Given mounting antimicrobial resistance and few anti-pseudomonals in development, there is a need for novel strategies to prevent ventilator-associated pneumonia (VAP) caused by Pseudomonas aeruginosa (PA), a common cause of death following trauma complicated by hemorrhagic shock (T/HS). We previously demonstrated in a rat model of T/HS that type I and II alveolar epithelial cells (AEC) undergo apoptosis, which is accompanied by a 50% reduction in surfactant protein-D (SPD). When intratracheal instillation of PA followed T/HS, PA bacterial burden increased 10 fold and PA pneumonia mortality increased 80%. T/HS-mediated AEC apoptosis, SPD reduction, and PA pneumonia susceptibility were prevented by IL-6 via a Stat3-dependent pathway. The basis for T/HS-induced impaired innate immunity and its prevention by IL-6-activated Stat3 is unknown. The unfolded protein response (UPR) alleviates endoplasmic reticulum (ER) stress in

secretory cells like AEC II and has recently been s hown to caus e apoptos is when ER stress is severe. We s ought to define the UPR's contribution T/HS-mediated AEC apoptosis and its prevention by IL-6.

Methods: Global UPR transcriptome analysis of the lung was performed using Affymetrix chips of 4 groups of rats: sham, T/HS, T/HS+IL-6, and T/HS+IL-6 pretreated with a Stat3 inhibitor. Via Ingenuity Pathway Analysis and GO database, we generated a UPR-associated genes entity list. Genespring was used to interpret the impact of T/HS and interventions on those mediators of the UPR.

Results: T/HS altered levels of 47% of UPR transcripts compared to sham ($p<0.05$, ANOVA). The pro-apoptotic UPR members, ATF4, CHOP, GADD34, Xbp1, and Eif2ak2 were upregulated in T/HS (1.5-4.7 fold; $p<0.05$, ANOVA). These transcripts were normalized in IL-6 treated animals in a Stat3-dependent manner ($p<0.05$, ANOVA).

Conclusion: Thus, the UPR transcriptome is significantly impacted by T/HS. Based on apoptotic effect, these findings suggest the UPR mediators CHOP, ATF4, Xbp1, GADD34, and Eif2ak2 may contribute the AEC apoptosis following T/HS, which is mitigated by IL-6 in a Stat3-dependent pathway. Using clinically available UPR modulators may prevent AEC apoptosis, thereby protecting against innate immune dysfunction of the lung and subsequent PA VAP following T/HS.

Title: Contribution of Heat Shock Proteins 70 and 40 to Prevention of Alveolar Epithelial Cell Apoptosis in Trauma Complicated by Hemorrhagic Shock

Stephen A Thacker, MD[1], Ana Moran, MD[2], Maria Huby, MD[2] and David J Tweardy, MD[2]. [1]Pediatrics, Section of Infectious Disease, Baylor College of Medicine, Houston, Texas, United States and [2]Internal Medicine, Section of Infectious Disease, Baylor College of Medicine, Houston, Texas, United States.

Background: Given mounting antimicrobial resistance and few anti-pseudomonals in development, there is a need for novel strategies to prevent ventilator-associated pneumonia (VAP) caused by Pseudomonas aeruginosa (PA), a common cause of death following trauma complicated by hemorrhagic shock (T/HS). We previously demonstrated in a rat model of T/HS that type I and II alveolar epithelial cells (AEC) undergo apoptosis, which is accompanied by a 50% reduction in surfactant protein-D (SPD). When intratracheal installation of PA followed T/HS, there was a 10-fold increase in PA bacterial burden and PA pneumonia mortality increased 80%. Notably, T/HS-mediated AEC apoptosis, SPD reduction, and PA pneumonia susceptibility were prevented by IL-6 via a Stat3-dependent pathway. The basis for T/HS-induced impaired innate immunity and its prevention by IL-6-activated Stat3 is unknown. The unfolded protein response (UPR) alleviates endoplasmic reticulum (ER) stress in secretory cells like AEC II when the stress is mild-to-moderate, but has recently been shown to cause apoptosis when ER stress is severe.

Objective: Determine the UPR's contribution T/HS-mediated AEC apoptosis and its prevention by IL-6.

Design/Methods: Global UPR transcriptome analysis was performed using Affymetrix chips of 4 groups of rats: sham, T/HS, T/HS+IL-6, and T/HS+IL-6 pretreated with a Stat3 inhibitor. Using Ingenuity Pathway Analysis© and GO database, we generated a list of 185 UPR-associated genes; 113 were annotated on the chip. Genespring© was used to interpret the impact of T/HS and interventions on those mediators of the UPR.

Results: T/HS altered levels of 30% of UPR transcripts compared to sham ($p<0.05$, ANOVA). All significantly dysregulated pro-apoptotic UPR transcripts normalized with IL-6. The protein folding chaperones, heat shock proteins 70 and 40 (Hsp70, Hsp40) were identified as the most dysregulated UPR mediators in T/HS (>25 fold and >9 fold, respectively; $p<0.05$, ANOVA). Hsp70 and Hsp40 were further upregulated >5 fold in T/HS+IL-6 animals and downregulated >9 fold in T/HS+IL-6

animals with Stat3 inhibition ($p<0.05$, ANOVA).

Conclusions: Thus, Hsp70 and Hsp40 play an adaptive role in T/HS-mediated AEC apoptosis that is augmented by IL-6 through a novel Stat3-dependent pathway. Increasing these chaperones within the lungs using clinically available proteostasis modulators may prevent AEC apoptosis and PA VAP following T/HS.

Title: Contribution of the Unfolded Protein Response to Prevention of Alveolar Epithelial Cell Apoptosis in Trauma Complicated by Hemorrhagic Shock

Stephen A Thacker, MD[1], Ana Moran, MD[2], Maria Huby, MD[2] and David J Tweardy, MD[2]. [1]Pediatrics, Section of Infectious Disease, Baylor College of Medicine, Houston, Texas, United States and [2]Internal Medicine, Section of Infectious Disease, Baylor College of Medicine, Houston, Texas, United States.

Given mounting antimicrobial resistance and few anti-pseudomonals in development, there is a need for novel strategies to prevent ventilator-associated pneumonia (VAP) caused by *Pseudomonas aeruginosa* (PA), a common cause of death following trauma complicated by hemorrhagic shock (T/HS). We previously demonstrated in a rat model of T/HS that type I and II alveolar epithelial cells (AEC) undergo apoptosis, which is accompanied by a 50% reduction in surfactant protein-D (SPD). When intratracheal instillation of PA followed T/HS, PA bacterial burden increased 10 fold and PA pneumonia mortality increased 80%. T/HS-mediated AEC apoptosis, SPD reduction, and PA pneumonia susceptibility were prevented by IL-6 via a Stat3-dependent pathway. The basis for T/HS-induced impaired innate immunity and its prevention by IL-6-activated Stat3 is unknown. The unfolded protein response (UPR) alleviates endoplasmic reticulum (ER) stress in secretory cells like AEC II and has recently been shown to cause apoptosis when ER stress is severe. We sought to define the UPR's contribution T/HS-mediated AEC apoptosis and its prevention by IL-6.

Global UPR transcriptome analysis of the lung was performed using Affymetrix chips of 4 groups of rats: sham, T/HS, T/HS+IL-6, and T/HS+IL-6 pretreated with a Stat3 inhibitor. Via Ingenuity Pathway Analysis and GO database, we generated a UPR-associated genes entity list. Genespring was used to interpret the impact of T/HS and interventions on those mediators of the UPR.

T/HS altered levels of 46% of UPR transcripts compared to sham ($p<0.05$, ANOVA). The pro-apoptotic UPR members, ATF4, CHOP, GADD34, Xbp1, and Eif2ak2 were upregulated in T/HS (1.5-4.7 fold; $p<0.05$, ANOVA). These transcripts were normalized in IL-6 treated animals in a Stat3-dependent manner ($p<0.05$, ANOVA).

Thus, the UPR transcriptome is significantly impacted by T/HS. Based on apoptotic effect, these findings suggest the UPR mediators CHOP, ATF4, Xbp1, GADD34, and Eif2ak2 may contribute the AEC apoptosis following T/HS, which is mitigated by IL-6 in a Stat3-dependent pathway. Using clinically available UPR modulators may prevent AEC apoptosis, thereby protecting against innate immune dysfunction of the lung and subsequent PA VAP following T/HS.

IMPACT OF TRAUMA/HEMORRHAGIC SHOCK ON THE UNFOLDED PROTEIN RESPONSE TRANSCRIPTOME OF THE HEART, LUNG, AND LIVER

Trauma is a major cause of mortality in the U.S. Those surviving initial trauma often succumb to multiple organ failure involving the liver, heart, and lung. Trauma with hemorrhagic shock (T/HS) has been shown to cause hepatocyte, cardiomyocyte, and alveolar epithelial cell apoptosis. IL-6 given at resuscitation was shown to prevent T/HS-induced apoptosis in these cells, and Stat3 largely mediated this. Specific genes contributing to apoptosis and its prevention; however, were not clearly delineated. Endoplasmic reticulum stress elicits the unfolded protein response (UPR), which, with marked activation, can lead to apoptosis. Prior studies of hepatic, cardiac, and pulmonary injury have examined a limited repertoire of the UPR, making it difficult to assess the maladaptive or inadequately adaptive role of the UPR in T/HS in these organs.

Global UPR transcriptome analysis was performed using Affymetrix chips of 4 groups of rats: sham, T/HS, T/HS+IL-6, and T/HS+IL-6 pretreated with a Stat3 inhibitor. Ingenuity Pathway Analysis and GO were used to create a UPR-associated gene list. Genespring was used to interpret the impact of T/HS and interventions on those UPR mediators.

T/HS significantly altered 12% of the UPR transcripts across all organs, with the most impacted canonical UPR members being DDIT3, GADD34, and ATF4 ($p<0.05$, ANOVA). T/HS also induced organ-specific UPR transcriptome changes, identifying the chaperone Hsp70 as the most dysregulated in the liver

and heart following T/HS (25 and 10 fold, respectively; $p<0.05$, ANOVA) and Eif2ak2 identified as the most dysregulated in the lung (4.7 fold; $p<0.05$, ANOVA). Hsp70 may contribute to hepatocyte protection via an IL-6-mediated Stat3-dependent pathway, identifying a potential novel therapeutic strategy to prevent hepatocyte death and organ dysfunction in T/HS.

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Increased apoptosis of peripheral blood neutrophils is associated with reduced incidence of infection in trauma patients with hemorrhagic shock

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KEYWORDS
Apoptosis;
Neutrophil;
Infection;
Trauma;
Shock;
Hemorrhage

Summary *Objective:* We aimed to describe the relationship between early peripheral leukocyte apoptosis and incidence of subsequent infection in trauma patients with hemorrhagic shock (T/HS).
Methods: T/HS patients requiring emergency surgery were prospectively enrolled. Nucleosome ELISA and TUNEL staining were performed on peripheral blood drawn pre-operatively, post-operatively and at 24 h. Subjects were followed for 30 days or until death or hospital discharge to record all episodes of infection.
Results: Forty-one subjects were enrolled. Six died within 24 h of surgery and were not included in the analysis. Nucleosome levels peaked post-operatively and dropped to baseline levels at 24 h ($p = 0.03$). TUNEL analysis revealed that polymorphonuclear neutrophils (PMNs) accounted for 72% of apoptotic leukocytes; the remaining apoptotic cells were mainly lymphocytes. Increased post-operative leukocyte apoptosis was associated with decreased systemic inflammatory response syndrome (SIRS) severity. Seventeen of the 35 survivors (48.6%) developed infections, while 18 (51.4%) did not. Pre-operative and post-operative nucleosome levels were 2.5 and 3 times higher, respectively, in T/HS patients who did not develop infection compared to those who did. Increased nucleosome levels were associated in particular with protection against sepsis ($p=0.03$) and multiple infections ($p = 0.01$).
Conclusion: Peripheral blood PMN apoptosis in the early resuscitative period is associated with decreased incidence of subsequent infection in T/HS patients.

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Introduction

Trauma continues to be an enormous public health problem and is a leading cause of death around the world.[1] In the United States, trauma is the fifth leading cause of death overall and the number one cause of death for individuals between the ages of 1 and 45 years.[2] With over 170,000 trauma deaths in the US in 2005, more Americans died of injuries than from cancers of the breast, colon, prostate, liver and pancreas combined.[3] Historically, the majority of trauma victims die before reaching the hospital[4]; however, more recent epidemiologic studies have shown that advances in trauma care systems and emergency medical services have resulted in a significantly larger percentage of patients who survive to hospital admission.[5] Although exsanguination and head injury continue to account for a large proportion of early trauma deaths, the majority of late trauma deaths occur as a result of infection and/or multiple organ failure (MOF).[5]

The clinical association between late trauma deaths and the development of MOF and infections has been well established since the 1970s.[6] However, it has primarily been in the past two decades or so that researchers have focused their investigations on the body's immunological and inflammatory responses to trauma-resuscitation at a molecular and cellular level in an effort to better understand MOF in this setting and how it predisposes to infections.

In addition to playing a key role in protection against acute bacterial infections, polymorphonuclear neutrophils (PMNs) modulate the innate immune response to non-infectious tissue insults such as trauma and shock. PMN apoptosis has been shown to be blunted in patients with SIRS[7] and sepsis[8,9] where it is thought to exacerbate tissue injury.[10] Reduced PMN apoptosis has been attributed, at least in part, to production of pro-inflammatory cytokines such as G-CSF that prolong PMN survival.[11–13] Further studies are needed to improve our understanding of the impact of altered PMN apoptosis on outcomes of trauma, particularly infections that complicate MOF.

We previously demonstrated in a rat model of trauma and hemorrhagic shock that cardiac,[14] hepatocyte,[15] alveolar epithelial cells[16] and PMN apoptosis (Tweardy et al., 2006, unpublished findings) are increased as a function of the duration of hypotensive phase and that apoptosis peaks approximately 4 h following initiation of resuscitation. In the current study, we examined the hypotheses that increased peripheral PMN apoptosis occurs early in the resuscitative period in trauma/hemorrhagic shock (T/HS) patients and is associated with a decreased incidence of infections. Our findings show that peripheral leukocyte apoptosis occurs in T/HS patients, achieves maximum levels immediately post-operatively and normalizes by 24 h. PMN were the predominant cell within the leukocyte population undergoing apoptosis. In addition, the degree of leukocyte apoptosis was inversely proportional to systemic inflammatory response syndrome (SIRS) severity and the risk of infection. These findings support the hypothesis that neutrophil apoptosis limits early tissue injury thereby decreasing subsequent susceptibility to infection in hospitalized T/HS patients.

Material and methods

Patient description and enrollment

This research was conducted at Ben Taub General Hospital, a level-one trauma center located in Houston, TX. Trauma patients arriving consecutively at the Emergency Center (EC) with a systolic blood pressure less than 90 mm Hg who required emergent laparotomy or thoracotomy were enrolled and brought immediately to the operating room (OR) where they underwent simultaneous fluid resuscitation and repair of their injuries. All samples and outcomes data were collected prospectively as part of a separate, ongoing randomized controlled clinical trial at our institution comparing hypotensive resuscitation to standard fluid resuscitation for T/HS patients.[17] Inclusion criteria for the study included traumatic injury to the chest and/or abdomen requiring emergent laparotomy or thoracotomy and at least one documented systolic blood pressure less than 90 mm Hg. Exclusion criteria included any of the following: (1) age $>$45 years or $<$14 years; (2) pregnancy; (3) incarceration; (4) known history of coronary artery disease, renal disease or cerebrovascular disease; (5) patients in whom traumatic brain injury could not be definitively ruled out based upon mechanism of injury and/or negative CT scan of the head. Patients enrolled in the clinical trial that fulfilled all the inclusion criteria and did not fulfill any exclusion criterion were enrolled in the study. In just over half the cases, emergent surgery was initiated before collection of the pre-operative blood sample could be done. Such patients were excluded from the study. Patients were followed daily for 30 days or until death or hospital discharge. Patients' vital signs and all incidences of infection were recorded.

Venous blood sampling and leukocyte apoptosis studies

Peripheral venous blood samples were drawn at three time points: pre-operatively, post-operatively, and at 24 h. Pre-operative samples were collected either in the EC or in the OR immediately preceding the start of the case; post-operative samples were drawn upon transfer from the OR to the surgical intensive care unit (SICU); and 24-h samples were drawn at 24 h after admission to the SICU. Timing of the immediate post-operative blood sample was based upon our previous finding that peak levels of cell apoptosis typically occur within 4 h of initiating fluid resuscitation following hemorrhagic shock in animals.[14–16] Five milliliters of blood was collected in two heparinized tubes. Peripheral blood leukocytes were harvested by dextran sedimentation, as previously described,[18] and the cell pellets immediately frozen for protein extraction. Protein was extracted using lysis buffer (Roche) and quantified using the Bradford method. Nucleosome ELISA was then performed using the Cell Death Detection ELISAplus® kit (Roche). In addition to the nucleosome ELISA assay, cytospins were prepared from leukocytes isolated from 8 of the post-operative blood samples and TUNEL stained as described.[14] The percentage of TUNEL-positive leukocytes, polymorphonuclear leukocytes (PMN) and mononuclear cells within each

sample was enumerated microscopically within 20 random 1000× fields by one of the authors (AM) experienced in blood cell histology.

Clinical data

Vital signs (heart rate, temperature, respiratory rate and blood pressure) were recorded for the entire study duration of 30 days or till discharge or death. Clinical outcomes of mortality and infection were also recorded. Infection was defined according to the criteria described in Table 1. Patient had to exhibit all the listed criteria in order to be diagnosed with infection. Culture positivity was included as one of the criteria for more stringent and accurate diagnosis. The association of peak post-operative nucleosome level with SIRS data collected at three definitive time points, namely pre-operative, post-operative and 24 h was analyzed for each participating patient in the study.

Statistical analysis

Statistical analysis was performed using STATA® statistical software package, version 10.0 (StataCorp, College Station, TX). Comparisons of continuous, independent variables were performed using the Wilcoxon–Mann–Whitney test. Comparisons of continuous, paired variables were performed using the Wilcoxon Signed Rank test.

Results

Peripheral blood leukocyte apoptosis peaks immediately post-operatively and consists mostly of neutrophils

Forty-one patients had post-operative blood samples drawn and were included in the study. The subjects' baseline characteristics and intra-operative fluid requirements are shown in Table 2. The high prevalence of racial minorities noted in this study roughly reflects the racial breakdown of penetrating trauma victims treated at our urban, county hospital. The mean time from presentation to the emergency center to arrival in the OR was 15.6 min. The mean duration of surgery was 114 min.

Nucleosome levels in study subjects peaked at the post-operative time point, and then dropped to pre-operative levels at 24 h (Fig. 1A). The 41% decrease of nucleosome levels at 24-h vs. the post-operative time point was statistically significant ($p = 0.03$); the 1.7-fold increase in post-operative nucleosome levels vs. pre-operative levels nearly reached statistical significance ($p = 0.06$).

TUNEL analysis was performed on eight consecutive post-operative peripheral blood samples in order to quantify the percent of leukocytes undergoing apoptosis and to identify the type of leukocytes undergoing apoptosis (polymorphonuclear neutrophils [PMNs] vs. mononuclear cells). Overall, 9% of all peripheral leukocytes were apoptotic; PMNs accounted for 72% of the apoptotic cells with remaining cells consisting of lymphocytes.

Table 1 Types of infections and criteria for their diagnosis.

Pneumonia
1. Infiltrate on chest X-ray
2. Positive sputum culture
3. Fever and/or leukocytosis
Intra-abdominal infection
1. Fluid collection requiring drainage
2. Fluid described as purulent
3. ± Positive culture
Bacteremia and sepsis
1. Positive blood cultures
2. Meets ≥2 SIRS criteria
Urinary tract infection
1. Positive urine culture and/or urinalysis
2. Fever and/or leukocytosis
Wound infection
1. Erythema and/or wound drainage
2. Fever and/or leukocytosis
3. ± Positive wound culture

Patients must exhibit all of the criteria listed for each diagnosis.

Peripheral blood leukocyte apoptosis is inversely correlated with SIRS criteria during early resuscitation

Using a linear regression model, we found that post-operative nucleosome levels were inversely correlated to heart rate at 24 h (Fig. 1B; correlation coefficient $r = -0.36$, $p = 0.02$) and at 48 h (Fig. 1C; $r = -0.39$, $p = 0.01$). Post-operative nucleosome levels also were inversely correlated to temperature at 48 h (Fig. 1D; $r = -0.38$, $p = 0.01$). No such correlations were seen when comparing pre-operative or 24-h nucleosome levels to heart rate or temperature. Respiratory rate was not included in this analysis since the vast majority of patients were sedated and intubated and many of these patients had no spontaneous respirations over the ventilator settings.

Higher peripheral blood PMN apoptosis in the early resuscitative period is associated with incidence of subsequent infection

Of the 41 subjects in whom post-operative samples were obtained, six died within 24 h of surgery. Of the 35 survivors, 17 (48.6%) developed an infection over the next 30 days, three of whom subsequently died. Infections were defined as listed in Table 1; the incidence of each type of infection is listed in Table 3. Nine of the 17 subjects who developed an infection had multiple (≥2) infections. The mean number of infections in those who developed any infection was 1.8 (range 1–5). Eighteen subjects who survived past the initial 48 h never developed any type of infection during the next 30 days. Of these patients, one subsequently died.

Table 2 Patient characteristics ($n = 41$).

Demographics			
	Infection	No infection	Total
Age (mean ± SD)	31.6 ± 10.1	33.8 ± 8.6	32.5 ± 9.3
% Male	92%	94%	93%
Black	47%	54%	51%
Hispanic	53%	42%	46%
Asian	0%	4%	2%
Mechanism			
Blunt trauma	0%	4%	2%
Gunshot wound	94%	63%	76%
Stab wound	6%	33%	22%
Presenting vital signs mean ± SD			
Systolic BP	80 ± 20	71.9 ± 26.8	75 ± 24
Diastolic BP	49 ± 20	34.7 ± 16.9	40 ± 19
Pulse	113 ± 18	98.7 ± 43	104 ± 36
Baseline labs mean ± SD			
Base deficit	−9.2 ± 4.7	−13.8 ± 7.7	−12.0 ± 7.0
Hemoglobin	29.9 ± 4.3	31.8 ± 7.1	31.1 ± 6.2
Glucose	201.8 ± 58.5	223 ± 99	214 ± 84
Injury severity score mean ± SD			
RTS[a]	10.2 ± 1.8	9.8 ± 6.2	10 ± 4.6
ISS[b]	23.8 ± 10.8	20.7 ± 12.9	22.0 ± 12
TRISS[c]	0.97 ± 0.02	0.81 ± 0.33	0.88 ± 0.27
IV fluids mean ± SD			
Crystalloid (mL)	3588 ± 2039	3350 ± 1861	3449 ± 1915
Colloid (mL)	912 ± 404	458 ± 405	646 ± 464
Transfusions mean ± SD			
PRBC's (mL)	1515 ± 1937	2521 ± 2725	2100 ± 2400
FFP (mL)	383 ± 559	516 ± 943	460 ± 800
Platelets	50 ± 140	118 ± 943	100 ± 210
Total transfusions	1985 ± 2419	3115 ± 3696	2660 ± 3250
Total inputs	6456 ± 3803	6963 ± 4640	6750 ± 4270

[a] Revised trauma score.
[b] Injury severity score.
[c] Trauma-injury severity score.

There were no statistically significant differences at baseline between those who developed an infection vs. those who did not develop any infection with regards to each of the characteristics shown in Table 2 ($p > 0.05$ for all comparisons), with the exception of colloid administration. Patients who developed infection received more colloid intra-operatively than those who did not develop infection (910 ml vs. 530 ml; $p = 0.01$). There was no significant difference between the infected and uninfected patient groups regarding pre or peri-operative antibiotic use. Also there was no significant association between the risk of developing infection and randomization group for the trial determining the impact of hypotensive resuscitation vs. standard fluid resuscitation.

Of note, subjects who did not develop any infection had 3-fold higher leukocyte nucleosome levels pre-operatively (40.2 mU/mg; Fig. 2) than those who did develop an infection (13.6 mU/mg; $p = 0.04$). In addition, those who did not develop infection had 2.5-fold higher leukocyte apoptosis level post-operatively (49.8 mU/mg; Fig. 2 and Table 4) compared to those who did develop infection (19.8 mU/mg, $p = 0.02$). Twenty-four-hour leukocyte apoptosis levels in the two groups were similar (Fig. 2). These results suggest that leukocyte apoptosis is associated with protection against subsequent infection. The finding of increased leukocyte apoptosis pre-operatively also suggests the possibility of a genetic component to apoptosis of an individual's leukocytes in response to severe trauma.

To determine if increased leukocyte apoptosis is associated with protection from a particular type of infection or from more severe infection, we compared post-operative nucleosome levels within subgroups of T/HS patients who

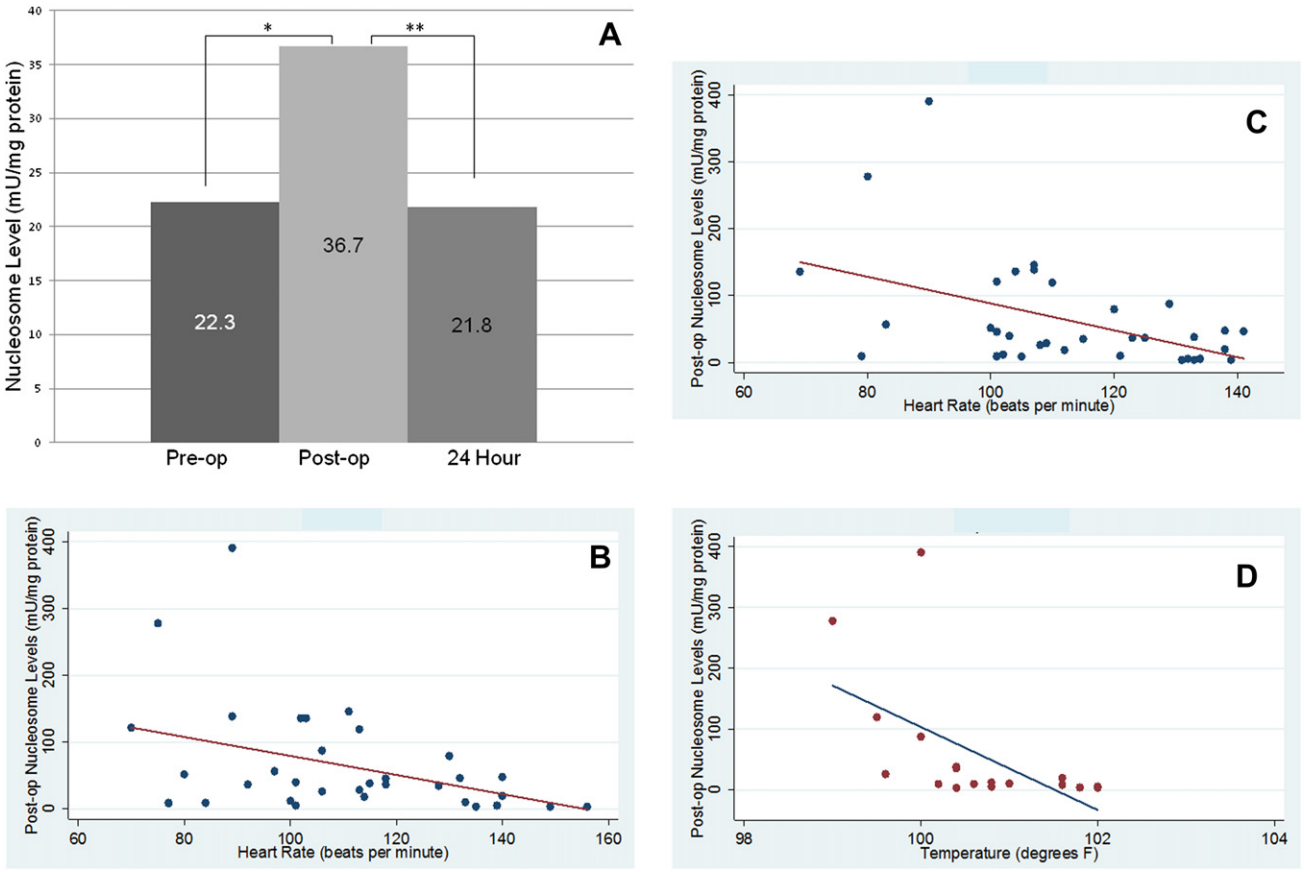

Figure 1 Peripheral blood leukocyte apoptosis peaks immediately post-operatively (A) and is inversely correlated with heart rate at 24 and 48 h (B, C) and temperature at 48 h (D) during early resuscitation. In panel A, peripheral blood was collected from patients at three time points—pre-op, post-op and 24 hours—for isolation of leukocytes by dextran sedimentation. Cells were lysed using buffer provided in the Cell Death Detection ELISAplus® kit (Roche) and protein quantified using the Bradford method. Nucleosome ELISA was then performed as described by the manufacturer (Roche) and each value normalized to total protein content with lysate. Data plotted are the median value for each time point (actual value indicated within each bar). Statistical differences between groups were determined using the Wilcoxon signed rank test; *p*-values are indicated by asterisks: (*) 0.06 and (**) 0.03. In panels B and C, post-operative peripheral blood leukocyte nucleosome levels were plotted as a function of heart rate at 24 h (B) or 48 h (C) for each patient. Post-operative nucleosome levels were inversely related to heart rate at 24 h ($r = -0.36$, $p = 0.02$) and 48 h ($r = -0.39$, $p = 0.01$; linear regression modeling). In panel D, post-operative peripheral leukocyte nucleosome levels were plotted as a function of temperature at 48 h for each patient. Post-operative peripheral leukocyte nucleosome levels were inversely related to temperature at 48 h ($r = -0.38$, $p = 0.01$; linear regression modeling).

developed particular types of infections, had multiple infections, or had bacteremia/sepsis with those who did not develop these complications (Table 4). Post-operative nucleosome levels in patients who did not develop bacteremia/sepsis were 4.2 fold higher than in those who did develop bacteremia/sepsis ($p = 0.03$), while post-operative nucleosome levels in patients who did not develop multiple infections were 4.6-fold higher than in those patients who did develop multiple infections ($p = 0.01$). These findings suggest that leukocyte apoptosis post-operatively is associated with protection from bacteremia/sepsis and multiple infections, in particular. Similar results suggest that higher

Table 3 Number of patients per infection category.

	n	% of Total subjects ($N = 35$)
Pneumonia	11	31
Intra-abdominal abscess	9	26
Bacteremia and sepsis	5	14
Urinary tract infection	4	11
Wound infection	4	11
Other (empyema)	1	3

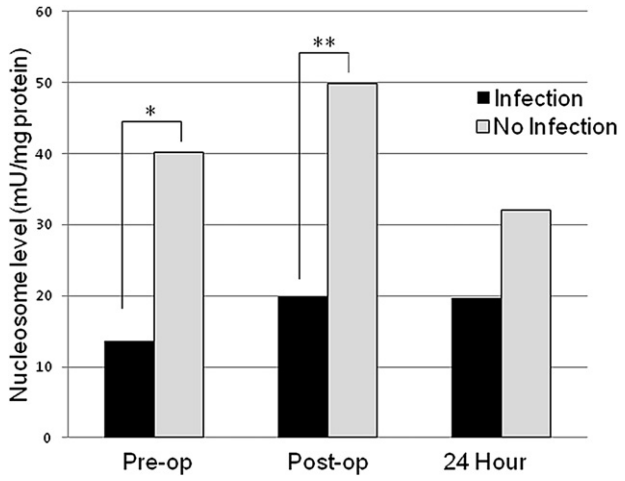

Figure 2 Peripheral blood leukocyte nucleosome levels in patients with and without infection. Peripheral blood was collected from patients at three time points—pre-op, post-op and 24 hours—for isolation of leukocytes by dextran sedimentation. Cells were lysed using buffer provided in the Cell Death Detection ELISAplus® kit (Roche) and protein quantified using the Bradford method. Nucleosome ELISA was then performed as described by the manufacturer (Roche) and each value normalized to total protein content with lysate. Patients were followed for 30 days, or until death or hospital discharge for development of infection. Pre-operative, post-operative and 24 h median nucleosome levels of patients who developed infection were compared to patients who did not develop any infection. Statistical differences between groups were determined using the Wilcoxon signed rank test; *p*-values are indicated by asterisks: (*) 0.04, (**) 0.02, and (***) >0.05.

leukocyte apoptosis pre-operatively is associated with protection from bacteremia/sepsis (data not shown).

Discussion

In this study, we demonstrated that peripheral leukocyte apoptosis occurs in T/HS patients, peaks immediately post-operatively, consists mostly of PMN, is inversely correlated with heart rate and fever at 24 and 48 h, and is higher pre-operatively and post-operatively in those destined to not develop infections, especially multiple infections and bacteremia plus sepsis. These results suggest that apoptosis of peripheral blood leukocytes, in particular PMN, early in hospitalized T/HS patients may protect patients from subsequent infection perhaps through reducing early PMN-mediated tissue injury.

Much of the disagreement in the literature over whether leukocyte apoptosis increases or decreases the risk of infection following hemorrhagic shock depends upon which leukocyte population is being examined. Studies involving lymphocytes have correlated increased levels of apoptosis within primary lymphoid organs such as the thymus and spleen with elevated risk of subsequent infection.[19–22] This is presumably due to the direct immunosuppressive effect of depleting functional lymphocytes within these organs. Regarding circulating blood lymphocytes, Teodorczyk-Injeyan et al suggested that injury related immune-deficiency correlated to increased T cell apoptosis.[23] Another recent study showed that high injury scores (SOFA) were linked to elevated circulating lymphocyte apoptosis markers (sFas, sFas/FAsL ratio) in patients with bacteremia.[24]

On the other hand, several studies of neutrophils in rodents have convincingly shown that increased levels of PMN apoptosis may actually reduce the severity of subsequent infection[25,26] and MOF.[10,27] Henrich et al suggest that trauma-activated PMNs release inflammatory mediators and contribute to tissue injury and delayed wound healing.[28]

Data from human studies are limited, and much remains to be learned. A recent study in trauma patients demonstrated an inverse correlation between degree of late neutrophil apoptosis and severity of end-organ dysfunction, however there was no significant difference between septic and non-septic patients.[29] The current study, to our knowledge, is the first to examine the impact of early peripheral blood PMN apoptosis on infectious outcomes in trauma patients with hemorrhagic shock. TUNEL staining of peripheral blood leukocyte cytospins in our current study demonstrated that 72% of the apoptotic leukocytes in the early post-operative period were PMNs. In keeping with these findings, and based upon other results presented in this paper, we propose that increased peripheral blood PMN apoptosis demonstrated early in the course of trauma-hemorrhagic shock may protect the severely injured trauma patient from developing subsequent infection, by one or both of two mechanisms. The first

Table 4 Correlation between post-operative nucleosome levels in peripheral blood leukocytes and type of infection.

	Infection		No infection		*p*-Value
	n	Median nucleosome level	*n*	Median nucleosome level	
Any infection	17	19.8	18	49.8	0.02[a]
Pneumonia	11	19.8	24	46.8	0.051
Abdominal abscess	9	26.1	26	39.0	0.57
Sepsis	5	10.2	30	42.8	0.03[a]
Urinary tract infection	4	14.2	31	39.8	0.07
Wound infection	4	27.4	31	39.8	0.19
Multiple infections	9	10.2	26	46.8	0.01[a]

[a] Analysis was performed using the Wilcoxon—Mann—Whitney test.

mechanism is through reducing immune-mediated tissue injury; the second mechanism involves restricted immunosuppression associated with clearance of apoptotic PMNs.

It is well established that PMNs play an integral role in the body's initial inflammatory response to trauma and are recruited to sites of injury.[6,10] Once sequestered, these cells possess tremendous potential to induce additional injury to the tissues to which they are recruited. Apoptotic PMNs within the circulation are removed by macrophages within the liver and spleen rather than infiltrating into organs and contributing to inflammation and further tissue injury. Preventing tissue injury and necrosis in this manner may reduce the risk that the organ will become a subsequent site of infection as well as the likelihood it will fail.

Tissue injury from infiltrating PMNs is not limited only to organs that have been directly injured from trauma. Ischemia-reperfusion injury (which occurs after successful resuscitation from hemorrhagic shock) also results in the recruitment of neutrophils to the reperfused organs. In fact, neutrophil-mediated organ injury following resuscitation from hemorrhage has been demonstrated in liver, heart, kidney, and intestine.[6] Additionally, activated PMNs stimulate macrophages to release inflammatory cytokines and chemotactic substances which further amplify the inflammatory response and increase the risk of developing MOF.[30] The presence of large numbers of activated PMNs has been repeatedly associated with pathogenesis of SIRS,[6,7,27] which itself is associated with increased risk of MOF and infection.[27,30] Patients with SIRS/MOF have been shown to have delayed PMN apoptosis,[7] enhanced PMN oxidative burst activity[7,10] and increased end-organ sequestration.[10] It therefore follows that if PMNs could be removed from the circulation before end-organ infiltration and therefore without inciting an inflammatory response, the risk of tissue injury and susceptibility to infection might be reduced.[26,27]

An alternative mechanism to explain our findings involves apoptosis-mediated immunosuppression. It is well established that apoptosis of PMN within tissue is accompanied by localized immunosuppression.[31,32] Ingestion of apoptotic cells by macrophages results in the release of anti-inflammatory mediators, including TGF-β1 and PGE_2[33] and suppresses the production of pro-inflammatory cytokines such as IL-8 and TNF-α, as well as other pro-inflammatory mediators, including TXA_2.[32] Clearance of circulating apoptotic PMNs by the liver and spleen may restrict immunosuppression to these organs thereby sparing other organs such as the lung, which is among the most common sites of infection following serious trauma that leads to MOF and death.

It is clear from the above discussion that neutrophils are a critical component of the innate host defense and their apoptosis and removal are essential for efficient resolution of inflammation. What remains unclear, however, is how PMN apoptosis is regulated in humans. A recent study demonstrated delayed spontaneous, as well as microbe-related apoptosis, of neutrophils in 4 patients with auto-inflammatory disease, leukocytosis, and single-nucleotide polymorphisms (SNPs) in two genes encoding proteins that contribute to the formation of the caspase-1-activating NALP3 inflammasome complex, *NLRP3* (Q705K) and *CARD8* (C10X).[34] These findings implicate these two genes as part of the genetic program controlling PMN apoptosis in response to stress and infection. A notable finding in our study was that infected and uninfected patients segregated early in the pre-operative course and exhibited a significant difference in pre-operative leukocyte apoptosis following severe injury. This finding suggests that it might be desirable to intervene early in those individuals with low pre-operative neutrophil apoptosis in an effort to increase it. However, such an intervention would need to be selective for neutrophils and otherwise safe.

A limitation of this study is the relatively small sample size, which makes it difficult to determine significant differences between subgroups of infected patients. In several instances, differences just barely failed to reach statistical significance, and it is possible that with a larger sample size, these differences might become statistically significant. Almost half of the patients in the parent trial were excluded from this study because surgery was initiated before collection of a pre-operative blood sample. This could be regarded as a potential limitation of the study, even though how it may have biased the results is unclear. Another limitation is the presence of numerous potential confounders, which could not be controlled for. Also, multiple comparisons between the infected and non-infected groups were made for the sake of completeness and the differences observed in neutrophil apoptosis between the groups may be due to the increased chance of a difference between groups emerging in the setting of multiple comparisons. The significance of identifying 72% of apoptotic cells as PMNs may have been enhanced if complete blood counts and differentials were also performed. Clearly, PMNs predominated as the most common apoptotic cell in the peripheral blood, but in the absence of peripheral blood leukocyte counts differentials, it is not possible to determine the absolute number of apoptotic PMN and lymphocytes.

In conclusion, this study demonstrates that increased peripheral blood PMN apoptosis in the early post-operative period is associated with decreased risk of developing subsequent infection in severely injured trauma patients requiring emergency laparotomy or thoracotomy. These findings add additional support to the hypothesis that strategies aimed at limiting PMN number and function at an early point in the course of resuscitation period may be beneficial in this patient population.

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None of the authors have any conflicts of interest to declare.

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